



Europäisches Patentamt  
European Patent Office  
Office européen des brevets



(11) **EP 1 327 680 A1**

(12) **EUROPEAN PATENT APPLICATION**  
published in accordance with Art. 158(3) EPC

(43) Date of publication:  
**16.07.2003 Bulletin 2003/29**

(51) Int Cl.7: **C12N 15/09**, C12N 15/62,  
C07K 16/28, A61K 39/395

(21) Application number: **01978851.2**

(86) International application number:  
**PCT/JP01/09259**

(22) Date of filing: **22.10.2001**

(87) International publication number:  
**WO 02/033072 (25.04.2002 Gazette 2002/17)**

(84) Designated Contracting States:  
**AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU  
MC NL PT SE TR**  
Designated Extension States:  
**AL LT LV MK RO SI**

(30) Priority: **20.10.2000 JP 2000321821**  
**17.04.2001 WOPCT/JP01/03288**  
**12.09.2001 JP 2001277314**

(71) Applicant: **CHUGAI SEIYAKU KABUSHIKI  
KAISHA**  
**Tokyo, 115-8543 (JP)**

(72) Inventors:  
• **TSUCHIYA, Masayuki,**  
**c/o CHUGAI SEIYAKU K.K.**  
**Gotemba-shi, Shizuoka 412-8513 (JP)**

- **OHTOMO, Toshihiko, c/o CHUGAI SEIYAKU K.K.**  
**Gotemba-shi, Shizuoka 412-8513 (JP)**
- **YABUTA, Naohiro, c/o CHUGAI SEIYAKU K.K.**  
**Niihari-gun, Ibaraki 300-4101 (JP)**
- **TSUNODA, Hiroyuki, c/o CHUGAI SEIYAKU K.K.**  
**Niihari-gun, Ibaraki 300-4101 (JP)**
- **ORITA, Tetsuro, c/o CHUGAI SEIYAKU K.K.**  
**Niihari-gun, Ibaraki 300-4101 (JP)**

(74) Representative: **HOFFMANN - EITLE**  
**Patent- und Rechtsanwälte**  
**Arabellastrasse 4**  
**81925 München (DE)**

(54) **DEGRADED TPO AGONIST ANTIBODY**

(57) The invention relates to a modified antibody which contains two or more H chain V regions and two or more L chain V regions of monoclonal antibody and can transduce a signal into cells by crosslinking TPO receptor to thereby exert TPO agonist action. The modified antibody can be used as a TPO signal transduction

agonist and, therefore, useful as a preventive and/or remedy for various diseases such as platelet-reduction-related blood diseases, thrombopenia following chemotherapy for cancer or leukemia, etc.

EP 1 327 680 A1

**Description****TECHNICAL FIELD**

**[0001]** This invention relates to modified antibodies containing two or more H chain V regions and two or more L chain V regions of an antibody which show TPO agonist activity by crosslinking TPO receptor. The modified antibodies have TPO agonist activity of transducing a signal into cells by crosslinking TPO receptor and are useful as a medicine for various purposes.

**BACKGROUND ART**

**[0002]** Thrombopoietin (TPO) is a platelet production regulation factor found in 1994 and is known to be composed of a glycoprotein having a molecular weight of 70-80 thousands produced mainly in liver. Thrombopoietin is a cytokine which in bone marrow promotes platelet precursor cells to survive, proliferate, differentiate and mature, namely promotes megakaryocytes to differentiate and proliferate. Thrombopoietin (TPO) receptor was identified earlier than TPO as c-Mpl, a receptor of a specific factor to regulate platelet production (M. Souyri et al., Cell 63: 1137 (1990)). It was reported that c-Mpl is distributed mainly in platelet precursor cells, megakaryocytes and platelet cells and that the suppression of c-Mpl expression inhibits selectively megakaryocyte formation (M. Methia et al., Blood 82: 1395 (1993)). It was reported that the ligand to c-Mpl is TPO based on the results of proliferation assay of cells specific to c-Mpl ligand and purification of the ligand using c-Mpl (F. de Sauvage et al., Nature 369: 533 (1994); TD. Bartley et al., Cell 77: 1117 (1994)). At present Mpl is called TPO receptor. Therefore TPO and TPO receptor agonists have been expected to work as a therapeutic agent for thrombocytopenia, for example, as a medicine alleviating thrombocytopenia caused by bone marrow inhibition or bone marrow resection therapy for cancer patients.

**[0003]** On the other hand modified antibodies, especially antibodies with lowered molecular size, for example, single chain Fvs were developed to improve permeability into tissues and tumors by lowering molecular size and to produce by a recombinant method. Recently the dimers of single chain Fvs, especially bispecific-dimers have been used for crosslinking cells. Typical examples of such dimers are hetero-dimers of single chain Fvs recognizing antigens of cancer cells and antigens of host cells like NK cells and neutrophils (Kipriyanov et al., Int. J. Cancer, 77, 9763-9772, 1998). They were produced by construction technique of single chain Fv as modified antibodies, which are more effective in treating cancers by inducing intercellular crosslinking. It has been thought that the intercellular crosslinking is induced by antibodies and their fragments (e.g. Fab fragment), bispecific modified antibodies and even dimers of single chain Fvs, which are monospecific.

**[0004]** As antibodies capable of transducing a signal by crosslinking a cell surface molecule(s), there are known an antibody against EPO receptor involved in cell differentiation and proliferation (JP-A 2000-95800), an antibody against MuSK receptor (Xie et al., Nature Biotech. 15, 768-771, 1997) and others. There are also known an agonist antibody to TPO receptor, its fragments and single chain Fvs (W099/17364). However there have been no reports on single chain Fv dimers and modified antibodies such as single chain bivalent antibodies having agonist activity.

**[0005]** Noticing that single chain Fv monomers derived from monoclonal antibodies (antibody MABL-1 and antibody MABL-2 produced by the inventors) which induce apoptosis of IAP-containing cells do not induce apoptosis of cells and that dimers induce apoptosis, the inventors discovered that dimers crosslink (dimerize) IAP receptor on cell surface, thereby a signal is transduced into the cells and, as a result, apoptosis is induced. This suggests that monospecific single chain Fv dimers crosslink a cell surface molecule(s) (e.g. receptor) and transduce a signal like a ligand, thereby serving as an agonist.

**[0006]** Focusing on the intercellular crosslinking, it was discovered that the above-mentioned single chain Fv dimers do not cause hemagglutination while the above-mentioned monoclonal antibodies do. The same result was also observed with single chain bivalent antibodies (single chain polypeptides containing two H chain V regions and two L chain V regions). This suggests that monoclonal antibodies may form intercellular crosslinking while modified antibodies like single chain Fv dimers and single chain bivalent antibodies crosslink a cell surface molecule(s) but do not form intercellular crosslinking.

**[0007]** Based on those observations the inventors have newly discovered that modified antibodies such as single chain Fv dimers and single chain bivalent antibodies crosslink a cell surface molecule(s) or intracellular molecule(s) of the same cell, in addition to known intercellular crosslinking, and are suitable as a ligand to the molecule(s) (especially as a ligand which mimics the action of natural ligand).

**[0008]** Discovering further that an antibody molecule (whole IgG) can be modified into single chain Fv dimers, single chain bivalent antibodies and the like which crosslink a cell surface molecule(s), thereby reducing side effects caused by intercellular crosslinking and providing new medicines inducing only desired effect on the cell, the inventors completed the invention. The modified antibodies of the invention have remarkably high activity compared with whole antibodies (IgG) having the same V region as the modified antibodies. They have an improved permeability into tissues

due to the lowered molecular size compared with antibody molecules and the lack of constant regions.

## DISCLOSURE OF INVENTION

**[0009]** An object of this invention is to provide low molecular-sized agonistic modified antibodies which contain two or more H chain V regions and two or more L chain V regions of a monoclonal antibody and have TPO agonist action by crosslinking TPO receptor.

**[0010]** Therefore, this invention relates the modified antibodies which contain two or more H chain V regions and two or more L chain V regions, preferably 2 to 6 each, especially preferably 2 to 4 each, most preferably two each, and show TPO agonist activity by crosslinking TPO receptor.

**[0011]** The "modified antibodies" in the specification mean any substances which contain two or more H chain V regions and two or more L chain V regions, wherein said V regions are combined directly or via linker through covalent bond or non-covalent bond. For example, polypeptides and compounds produced by combining each V region of antibody through a peptide linker or a chemical crosslinking agent and the like. Two or more H chain V regions and two or more L chain V regions used in the invention can be derived from the same antibody or from different antibodies.

**[0012]** Modified antibodies of the invention can be any things as long as they specifically recognize and crosslink TPO receptor and thereby can transduce a signal into cells. They include modified antibodies produced by further modifying a part of the amino acid sequence of V region of the modified antibodies.

**[0013]** Preferable examples of the modified antibodies of the invention are multimers such as dimers, trimers or tetramers of single chain Fv containing an H chain V region and an L chain V region, or single chain polypeptides containing two or more H chain V regions and two or more L chain V regions. When the modified antibodies of the invention are multimers of single chain Fv such as dimers, trimers, tetramers and the like containing an H chain V region and an L chain V region, it is preferable that the H chain V region and L chain V region existing in the same chain are not associated to form an antigen-binding site.

**[0014]** More preferable examples are dimers of the single chain Fv which contains an H chain V region and an L chain V region, or a single chain polypeptide containing two H chain V regions and two L chain V regions. The H chain V region and L chain V region are connected preferably through a linker in the modified antibodies.

**[0015]** The above-mentioned single chain Fv multimer includes a multimer by non-covalent bond, a multimer by a covalent bond through a crosslinking radical and a multimer through a crosslinking reagent (an antibody, an antibody fragment, or bivalent modified antibody). Conventional crosslinking radicals used for crosslinking peptides can be used as the crosslinking radicals to form the multimers. Examples are disulfide crosslinking by cysteine residue, other crosslinking radicals such as C<sub>4</sub> - C<sub>10</sub> alkylene (e.g. tetramethylene, pentamethylene, hexamethylene, heptamethylene and octamethylene, etc.) or C<sub>4</sub> - C<sub>10</sub> alkenylene (cis/trans -3-butenylene, cis/trans-2-pentenylene, cis/trans-3-pentenylene, cis/trans-3-hexenylene, etc.).

**[0016]** Moreover, the crosslinking reagent which can combine with a single chain Fv is, for example, an amino acid sequence which can optionally be introduced into Fv, for example, an antibody against FLAG sequence and the like or a fragment thereof, or a modified antibody originated from the antibody, for example, single chain Fv.

**[0017]** "TPO agonist action" in the specification means a biological action occurring in the cell(s) into which a signal is transduced by crosslinking TPO receptor, for example, proliferation, differentiation or growth stimulation of megakaryocytes, or platelet production.

**[0018]** ED50 of the TPO agonist action in the invention is determined by known methods for measuring agonist action. Examples for measurement are cell proliferation assay using TPO sensitive cell lines such as BaF/mpl or UT7/TPO, measurement of phosphorylation of MPL protein, megakaryocyte colony assay by differentiation from bone marrow cells, *in vivo* mouse platelet recovery synthesis assay, measurement of expression induction of platelet antigen GPIIb/IIIa (anti GPIIb/IIIa) using human leukemia megakaryoblastic cell line (CMK) or measurement of polyploidy induction of megakaryoblastic cell line (DAMI). ED50 is a dose needed for achieving 50% reaction of the maximum activity set as 100% in the dose-reaction curve.

**[0019]** Preferable modified antibodies of the invention have TPO agonist action (ED50) equivalent to or better than that of an antibody having the same antigen-binding region as the modified antibody, namely the whole antibody (hereinafter "parent antibody") like IgG having the same pair of H chain V region and L chain V region as the pair of H chain V region and L chain V region forming antigen-binding region of the modified antibody. More preferable are those having TPO agonist action (ED50) more than two times higher than that of parent antibody, further preferably more than 5 times, most preferably more than 10 times. The invention includes modified antibodies with TPO agonist action containing H chain V region and L chain V region forming the same antigen-binding region as the parent antibody which binds to TPO receptor but has no TPO agonist action to the molecule.

**[0020]** The compounds containing two or more H chain V regions and two or more L chain V regions of the invention can be any compounds which contain two or more H chain V regions and two or more L chain V regions of antibody and show TPO agonist action (ED50) equivalent to or better than that of thrombopoietin (TPO). Preferable are those

having TPO agonist action (ED50) more than two times higher than that of TPO, more preferably more than 5 times, most preferably more than 10 times.

**[0021]** The "compounds" mentioned here include not only modified antibodies of the invention but also any compounds containing two or more, preferably from 2 to 6, more preferably from 2 to 4, most preferably 2 antigen-binding regions such as whole antibodies or F(ab')<sub>2</sub>.

**[0022]** Preferable modified antibodies or compounds of the invention containing two or more H chain V regions and two or more L chain V regions of antibody have an intercellular adhesion action (ED50) not more than 1/10 compared with the parent antibody, more preferably have no substantial intercellular adhesion action.

**[0023]** ED50 of the intercellular adhesion action mentioned in the above is determined by known methods for measuring intercellular adhesion action, for example, by the measurement of agglomeration of cells expressing TPO receptor.

**[0024]** The invention relates to DNAs which code for the modified antibodies.

**[0025]** The invention relates to animal cells or microorganisms which produce the modified antibodies.

**[0026]** The invention relates to use of the modified antibody as TPO agonist.

**[0027]** The invention relates to a method of transducing a signal into cells by crosslinking TPO receptor using the modified antibody and thereby inducing TPO agonist action such as proliferation, differentiation-induction or growth stimulation of megakaryocytes, platelet production, phosphorylation of TPO receptor protein and the like.

**[0028]** The invention relates to a medicine for treating thrombocytopenia etc. containing the modified antibody as active component.

**[0029]** The invention relates to use of the modified antibody as a medicine.

**[0030]** The invention relates to a method of screening or measuring the modified antibody, which contains two or more H chain V regions and two or more L chain V regions of antibody and shows TPO agonist action by crosslinking TPO receptor, that comprises 1) to prepare a modified antibody containing two or more H chain V regions and two or more L chain V regions of antibody and binding specifically to TPO receptor, 2) to contact the modified antibody with cells expressing TPO receptor and 3) to measure TPO agonist action which occurs in the cells by crosslinking TPO receptor. The method of measurement is useful for the quality control in producing the modified antibodies of the invention as a medicine and other purposes.

**[0031]** The modified antibodies can be mono-specific modified antibodies or multi-specific modified antibodies like bi-specific modified antibodies. Preferable are mono-specific modified antibodies.

**[0032]** The present invention also relates to modified antibodies whose H chain V region and/or L chain V region is H chain V region derived from human antibody and/or L chain V region derived from human antibody. The H chain V region and/or L chain V region derived from human antibody can be obtained by screening human monoclonal antibody library as described in WO99/10494. The H chain V region and L chain V region derived from human monoclonal antibodies produced by transgenic mouse and the like are also included.

**[0033]** The present invention further relates to modified antibodies whose H chain V regions and/or L chain V regions are humanized H chain V regions and/or humanized L chain V regions. Specifically, the humanized modified antibodies consist of the humanized L chain V region which comprises framework regions (FR) derived from an L chain V region of human monoclonal antibody and complementarity determining regions (hereinafter "CDR") derived from an L chain V region of non-human mammalian (e.g. mouse, rat, bovine, sheep, ape) monoclonal antibody and/or the humanized H chain V region which comprises FR derived from an H chain V region of human monoclonal antibody and CDR derived from an H chain V region of non-human mammalian (e.g. mouse, rat, bovine, sheep, ape) monoclonal antibody. In this case, the amino acid sequences of CDR and FR may be partially altered, e.g. deleted, replaced or added.

**[0034]** H chain V regions and/or L chain V regions of the modified antibodies of the invention can be H chain V regions and/or L chain V regions derived from monoclonal antibodies of animals other than human (such as mouse, rat, bovine, sheep, ape, chicken and the like). In this case, the amino acid sequences of CDR and FR may be partially altered, e.g. deleted, replaced or added.

**[0035]** The invention also relates to DNAs encoding the various modified antibodies as mentioned above and genetic engineering techniques for producing recombinant vectors comprising the DNAs.

**[0036]** The invention also relates to host cells transformed with the recombinant vectors. Examples of host cells are animal cells such as human cells, mouse cells or the like and microorganisms such as *E. coli*, *Bacillus subtilis*, yeast or the like.

**[0037]** The invention relates to a process for producing the modified antibodies, which comprises culturing the above-mentioned hosts and extracting the modified antibodies from the culture thereof.

**[0038]** The present invention further relates to a process for producing a dimer of the single chain Fv which comprises culturing host animal cells producing the single chain Fv in a serum-free medium to secrete the single chain Fv into the medium and isolating the dimer of the single chain Fv formed in the medium.

**[0039]** The present invention also relates to the use of the modified antibodies as TPO agonist. That is, it relates to a signal-transduction agonist which comprises as an active ingredient the modified antibody obtained as mentioned in

the above.

**[0040]** Therefore, the pharmaceutical preparations containing TPO agonist modified antibodies of the invention as an active ingredient are useful as preventives and/or remedies for platelet-reduction-related blood diseases, thrombocytopenia caused by chemotherapy of cancers or leukemia, and the like.

**[0041]** The modified antibodies of the present invention comprise two or more H chain V regions and two or more L chain V regions derived from antibodies. The structure of the modified antibodies may be a dimer of single chain Fv comprising one H chain V region and one L chain V region or a polypeptide comprising two H chain V regions and two L chain V regions. In the modified antibodies of the invention, the V regions of H chain and L chain are preferably linked through a peptide linker which consists of one or more amino acids. The resulting modified antibodies contain variable regions of antibodies and bind to the antigen with the same specificity as that of the original monoclonal antibodies.

H chain V region

**[0042]** In the present invention, the H chain V region derived from an antibody recognizes TPO receptor and oligomerizes, for example, dimerizes through crosslinking said molecule, and thereby transduces a signal into the cells. The H chain V region of the invention includes H chain V regions derived from a mammal (e.g. human, mouse, rat, bovine, sheep, ape etc.) and H chain V regions having partially modified amino acid sequences of the H chain V regions. More preferable is a humanized H chain V region containing FR of H chain V region of a human monoclonal antibody and CDR of H chain V region of a mouse monoclonal antibody. Also preferable is an H chain V region having an amino acid sequence derived from a human, which can be produced by recombination technique. The H chain V region of the invention may be a fragment of aforementioned H chain V region, which fragment preserves the antigen binding capacity.

L chain V region

**[0043]** In the present invention, the L chain V region recognizes TPO receptor and oligomerizes, for example, dimerizes through crosslinking said molecule, and thereby transduces a signal into the cells. The L chain V region of the invention includes L chain V regions derived from a mammal (e.g. human, mouse, rat, bovine, sheep, ape etc.) and L chain V regions having partially modified amino acid sequences of the L chain V regions. More preferable is a humanized L chain V region containing FR of L chain V region of human monoclonal antibody and CDR of L chain V region of mouse monoclonal antibodies. Also preferable is an L chain V region having an amino acid sequence derived from a human, which can be produced by recombination technique. The L chain V regions of the invention may be fragments of L chain V region, which fragments preserve the antigen binding capacity.

Complementarity determining region (CDR)

**[0044]** Each V region of L chain and H chain forms an antigen-binding site. The variable region of the L and H chains is composed of comparatively conserved four common framework regions linked to three hypervariable regions or complementarity determining regions (CDR) (Kabat, E.A. et al., "Sequences of Protein of Immunological Interest", US Dept. Health and Human Services, 1983).

**[0045]** Major portions in the four framework regions (FRs) form  $\beta$ -sheet structures and thus three CDRs form a loop. CDRs may form a part of the  $\beta$ -sheet structure in certain cases. The three CDRs are held sterically close position to each other by FR, which contributes to the formation of the antigen-binding site together with three CDRs.

**[0046]** These CDRs can be identified by comparing the amino acid sequence of V region of the obtained antibody with known amino acid sequences of V regions of known antibodies according to the empirical rule in Kabat, E.A. et al., "Sequences of Protein of Immunological Interest". Single chain Fv

**[0047]** A single chain Fv is a polypeptide monomer comprising an H chain V region and an L chain V region linked each other which are derived from antibodies. The resulting single chain Fvs contain variable regions of the original antibodies and preserve the complementarity determining region thereof, and therefore the single chain Fvs bind to the antigen by the same specificity as that of the original antibodies (JP-Appl. 11-63557). A part of the variable region and/or CDR of the single chain Fv of the invention or a part of the amino acid sequence thereof may be partially altered, for example, deleted, replaced or added. The H chain V region and L chain V region composing the single chain Fv of the invention are mentioned before and may be linked directly or through a linker, preferably a peptide linker. The constitution of the single chain Fv may be [H chain V region]-[L chain V region] or [L chain V region]-[H chain V region]. In the present invention, it is possible to make the single chain Fv to form a dimer, a trimer or a tetramer, from which the modified antibody of the invention can be formed.

## Single chain modified antibody

**[0048]** The single chain modified antibodies of the present invention comprising two or more H chain V regions and two or more L chain V regions, preferably each two to four, especially preferable each two, comprise two or more H chain V regions and L chain V regions as mentioned above. Each region of the peptide should be arranged such that the modified single chain antibody forms a specific steric structure, concretely mimicking a steric structure formed by the dimer of single chain Fv. For instance, the V regions are arranged in the order of the following manner:

[H chain V region]-[L chain V region]-[H chain V region]-[L chain V region]; or  
[L chain V region]-[H chain V region]-[L chain V region]-[H chain V region],

wherein these regions are connected through a peptide linker, respectively.

## Linker

**[0049]** In this invention, the linkers for the connection between the H chain V region and the L chain V region may be any peptide linker which can be introduced by the genetic engineering procedure or any linker chemically synthesized. For instance, linkers disclosed in literatures, e.g. Protein Engineering, 9(3), 299-305, 1996 may be used in the invention. These linkers can be the same or different in the same molecule. If peptide linkers are required, the following are cited as example linkers:

Ser

Gly-Ser

Gly-Gly-Ser

Ser-Gly-Gly

Gly-Gly-Gly-Ser

Ser-Gly-Gly-Gly

Gly-Gly-Gly-Gly-Ser

Ser-Gly-Gly-Gly-Gly

Gly-Gly-Gly-Gly-Gly-Ser

Ser-Gly-Gly-Gly-Gly-Gly

Gly-Gly-Gly-Gly-Gly-Gly-Ser

Ser-Gly-Gly-Gly-Gly-Gly-Gly

(Gly-Gly-Gly-Gly-Ser)<sub>n</sub> and

(Ser-Gly-Gly-Gly-Gly)<sub>n</sub>

wherein n is an integer not less than one. Preferable length of the linker peptide varies dependent upon the receptor to be the antigen, in the case of single chain Fvs, the range of 1 to 20 amino acids is normally preferable. In the case of single chain modified antibodies comprising two or more H chain V regions and two or more L chain V regions, the peptide linkers connecting those forming the same antigen binding site comprising [H chain V region]-[L chain V region] (or [L chain V region]-[H chain V region]) have lengths of 1 - 30 amino acids, preferably 1 - 20 amino acids, more preferably 3 - 18 amino acids. The peptide linkers connecting those not forming the same antigen binding site comprising [H chain V region]-[L chain V region] or ([L chain V region]-[H chain V region]) have lengths of 1 - 40 amino acids, preferably 3 - 30 amino acids, more preferably 5 - 20 amino acids. The method for introducing those linkers will be

described in the explanation for DNA construction coding for modified antibodies of the invention.

**[0050]** The chemically synthesized linkers, i.e. the chemical crosslinking agents, according to the invention can be any linkers conventionally employed for the linkage of peptides. Examples of the linkers may include N-hydroxy succinimide (NHS), disuccinimidyl suberate (DSS), bis(sulfosuccinimidyl)suberate (BS<sup>3</sup>), dithiobis(succinimidyl propionate) (DSP), dithiobis(sulfosuccinimidyl propionate) (DTSSP), ethylene glycolbis(succinimidyl succinate) (EGS), ethylene glycolbis(sulfosuccinimidyl succinate) (sulfo-EGS), disuccinimidyl tartrate (DST), disulfosuccinimidyl tartrate (sulfo-DST), bis [2- (succinimido oxycarbonyloxy) ethyl]sulfone (BSOCOES), bis[2-(sulfosuccinimido oxycarbonyloxy) ethyl]sulfone (sulfo-BSOCOES) or the like. These are commercially available. It is preferable for the chemically synthesized linkers to have the length equivalent to that of peptide linkers.

**[0051]** To form a dimer of the single chain Fv it is preferable to select a linker suitable to dimerize in the solution such as culture medium more than 20%, preferably more than 50%, more preferably more than 80%, most preferably more than 90% of the single chain Fv produced in the host cells. Specifically, preferable is a linker composed of 2 to 12 amino acids, preferably 3 to 10 amino acids or other linkers corresponding thereto.

#### Preparation of modified antibodies

**[0052]** The modified antibodies can be produced by connecting, through the aforementioned linker, an H chain V region and an L chain V region derived from known or novel antibodies specifically binding to TPO receptor. As examples of the single chain Fvs are cited those having H chain V region and L chain V region of antibody 12B5 and antibody 12E10 described in WO99/10494. As examples of the modified antibodies of the invention having two or more H chain V regions and two or more L chain V regions are cited sc12B5 dimer (linker: 15 amino acids), sc12E10 dimer (linker: 15 amino acids), db12B5 dimer (linker: 5 amino acids), db12E10 dimer (linker: 5 amino acids), sc12B5sc(FV)<sub>2</sub> and sc12E10sc(FV)<sub>2</sub> which contain H chain V regions and L chain V regions derived from the above-mentioned monoclonal antibodies.

**[0053]** For the preparation of the modified antibodies, a signal peptide may be attached to its N-terminal if the polypeptide is desired to be a secretory peptide. A well-known amino acid sequence useful for the purification of polypeptide such as the FLAG sequence may be attached for the efficient purification of the polypeptide. In this case a dimer can be formed by using anti-FLAG antibody.

**[0054]** For the preparation of the modified antibody of the invention, it is necessary to obtain a DNA, i.e. a DNA encoding the single chain Fv or a DNA' encoding reconstructed single chain polypeptide. These DNAs, especially for sc12B5, db12B5, sc12E10 and/or db12E10 are obtainable from the DNAs encoding the H chain V regions and the L chain V regions derived from said Fvs. They are also obtainable by polymerase chain reaction (PCR) method using those DNAs as a template and amplifying the part of DNA contained therein encoding desired amino acid sequence with the aid of a pair of primers corresponding to both ends thereof.

**[0055]** In the case where each V region having partially modified amino acid sequence is desired, the V regions in which one or some amino acids are modified, i.e. deleted, replaced or added can be obtained by a procedure known in the art using PCR. A part of the amino acid sequence in the V region is preferably modified by the PCR known in the art in order to prepare the modified antibody which is sufficiently active against the specific antigen.

**[0056]** For the determination of primers for the PCR amplification, the types of H chain and L chain, if a monoclonal antibody is used as a starting material, are determined by a typing method known in the technical field.

**[0057]** For the amplification of the L chain V regions of antibody 12B5 and antibody 12E10 by PCR, 5'-end and 3'-end oligonucleotide primers are decided as aforementioned. In the same manner, 5'-end and 3'-end oligonucleotide primers are decided for the amplification of the H chain V regions of antibody 12B5 and antibody 12E10.

**[0058]** In embodiments of the invention, the 5'-end primers which contain a sequence "GATC" providing the restriction enzyme Hinf I recognition site at the neighborhood of 5'-terminal thereof are used and the 3'-end primers which contain a nucleotide sequence "CCCGGG" providing the XmaI recognition site at the neighborhood of 5'-terminal thereof are used. Other restriction enzyme recognition site may be used instead of these sites as long as they are used for subcloning a desired DNA fragment into a cloning vector.

**[0059]** Specifically designed PCR primers are employed to provide suitable nucleotide sequences at 5'-end and 3'-end of the cDNAs encoding the V regions of the antibodies 12B5 and 12E10 so that the cDNAs are readily inserted into an expression vector and appropriately function in the expression vector (e.g. this invention devises to increase transcription efficiency by inserting Kozak sequence). The V regions of the antibodies 12B5 and 12E10 obtained by amplifying by PCR using these primers are inserted into HEF expression vector containing the desired human C region (see W092/19759). The cloned DNAs can be sequenced by using any conventional process, for example, by the automatic DNA sequencer (Applied Biosystems).

**[0060]** A linker such as a peptide linker can be introduced into the modified antibody of the invention in the following manner. Primers which have partially complementary sequence with the primers for the H chain V regions and the L chain V regions as described above and which code for the N-terminal or the C-terminal of the linker are designed.

Then, the PCR procedure can be carried out using these primers to prepare a DNA encoding the peptide linker having desired amino acid sequence and length. The DNAs encoding the H chain V region and the L chain V region can be connected through the resulting DNA to produce the DNA encoding the modified antibody of the invention which has the desired peptide linker. Once the DNA encoding one of the modified antibodies is prepared, the DNAs encoding the modified antibodies with or without the desired peptide linker can readily be produced by designing various primers for the linker and then carrying out the PCR using the primers and the aforementioned DNA as a template.

**[0061]** Each V region of the modified antibody of the present invention can be humanized by using conventional techniques (e.g. Sato, K. et al., Cancer Res., 53, 1-6 (1993)). Once a DNA encoding each of humanized Fvs is prepared, a humanized single chain Fv, a fragment of the humanized single chain Fv, a humanized monoclonal antibody and a fragment of the humanized monoclonal antibody can readily be produced according to conventional methods. Preferably, amino acid sequences of the V regions thereof may be partially modified, if necessary.

**[0062]** Furthermore, a DNA derived from other mammalian origin, for example a DNA encoding each of V regions of human antibody, can be produced in the same manner as used to produce DNA encoding the H chain V region and the L chain V region derived from mouse by conventional methods as mentioned in the above. The resulting DNA can be used to prepare an H chain V region and an L chain V region of other mammal, especially derived from human antibody, a single chain Fv derived from human and a fragment thereof, and a monoclonal antibody of human origin and a fragment thereof.

**[0063]** When the modified antibodies of the invention is bi-specific modified antibodies, they can be produced by known methods (for example, the method described in W09413804).

**[0064]** As mentioned above, when the aimed DNAs encoding the V regions of the modified antibodies and the V regions of the humanized modified antibodies are prepared, the expression vectors containing them and hosts transformed with the vectors can be obtained according to conventional methods. Further, the hosts can be cultured according to a conventional method to produce the reconstructed single chain Fv, the reconstructed humanized single chain Fv, the humanized monoclonal antibodies and fragments thereof. They can be isolated from cells or a medium and can be purified into a homogeneous mass. For this purpose any isolation and purification methods conventionally used for proteins, e.g. chromatography, ultra-filtration, salting-out and dialysis, may be employed in combination, if necessary, without limitation thereto..

**[0065]** When the reconstructed single chain Fv of the present invention is produced by culturing an animal cell such as COS7 cells or CHO cells, preferably CHO cells, in a serum-free medium, the dimer of said single chain Fv formed in the medium can be stably recovered and purified in a high yield. Thus purified dimer can be stably preserved for a long period. The serum-free medium employed in the invention may be any medium conventionally used for the production of a recombinant protein without limit thereto.

**[0066]** For the production of the modified antibodies of the present invention, any expression systems can be employed, for example, eukaryotic cells such as animal cells, e.g., established mammalian cell lines, filamentous fungi and yeast, and prokaryotic cells such as bacterial cells e.g., *E. coli*. Preferably, the modified antibodies of the invention are expressed in mammalian cells, for example COS7 cells or CHO cells.

**[0067]** In these cases, conventional promoters useful for the expression in mammalian cells can be used. Preferably, human cytomegalovirus (HCMV) immediate early promoter is used. Expression vectors containing the HCMV promoter include HCMV-VH-HCγ 1, HCMV-VL-HCK and the like which are derived from pSV2neo (W092/19759).

**[0068]** Additionally, other promoters for gene expression in mammal cell which may be used in the invention include virus promoters derived from retrovirus, polyoma virus, adenovirus and simian virus 40 (SV40) and promoters derived from mammal such as human polypeptide-chain elongation factor-1α (HEF-1α). SV40 promoter can easily be used according to the method of Mulligan, R.C., et al. (Nature 277, 108-114 (1979)) and HEF-1α promoter can also be used according to the methods of Mizushima, S. et al. (Nucleic Acids Research, 18, 5322 (1990)).

**[0069]** Replication origin (ori) which can be used in the invention includes ori derived from SV40, polyoma virus, adenovirus, bovine papilloma virus (BPV) and the like. An expression vector may contain, as a selection marker, phosphotransferase APH (3') II or I (neo) gene, thymidine kinase (TK) gene, *E. coli* xanthine-guanine phosphoribosyl transferase (Ecogpt) gene or dihydrofolate reductase (DHFR) gene.

**[0070]** The antigen-binding activity of the modified antibody prepared in the above can be evaluated by a conventional method such as radio immunoassay (RIA), enzyme-linked immunosorbent assay (ELISA) or surface plasmon resonance. It can also be evaluated using the binding-inhibitory ability of original antibody as an index, for example in terms of the absence or presence of concentration-dependent inhibition of the binding of said monoclonal antibody to the antigen.

**[0071]** More in detail, animal cells transformed with an expression vector containing a DNA encoding the modified antibody of the invention, e.g., COS7 cells or CHO cells, are cultured. The cultured cells and/or the supernatant of the medium or the modified antibody purified from them are used to determine the binding to antigen. As a control is used a supernatant of the culture medium in which cells transformed only with the expression vector were cultured. In the case of an antigen, for example, the antibody 12B5 and the antibody 12E10, a test sample of the modified antibody of

the invention or a supernatant of the control is added to Ba/F3 cells expressing human MPL and then an assay such as the flow cytometry is carried out to evaluate the antigen-binding activity.

[0072] In vitro evaluation of the signal transduction effect (for example, proliferation, differentiation-induction or growth stimulation of megakaryocyte, platelet production, or phosphorylation of TPO receptor protein) is performed in the following manner. A test sample of the above-mentioned modified antibody is added to the cells which are expressing the antibody or cells into which the gene for the antibody has been introduced, and is evaluated by the change caused by the signal transduction (for example, human MPL antigen-specific proliferation, measurement of protein phosphorylation, or expression of platelet-specific antigen) using conventional methods.

[0073] In vivo evaluation is carried out by administering a monoclonal antibody recognizing MPL, a modified antibody of the invention and PBS as control to mice, and evaluating the strength of the activity by the change of the amount of platelet in mouse serum.

[0074] As mentioned above the modified antibodies of the invention can be obtained by preparing modified antibodies which contain two or more H chain V regions and two or more L chain V regions and specifically bind to TPO receptor and screening the modified antibodies by in vivo or in vitro evaluation as mentioned in the above.

[0075] The modified antibodies of the invention, which comprises two or more H chain V regions and two or more L chain V regions, preferably each two to four, more preferably each two, may be a dimer of the single chain Fv comprising one H chain V region and one L chain V region, or a single chain polypeptide in which two or more H chain V regions and two or more L chain V regions are connected. It is considered that owing to such construction the peptide mimics three dimensional structure of TPO and therefore retains an excellent antigen-binding property and TPO agonist activity.

[0076] The modified antibodies of the invention have a remarkably lowered molecular size compared with parent antibody molecule (e.g. IgG), and, therefore, have a superior permeability into tissues and tumors and a higher activity than parent monoclonal antibody molecule. Therefore, the modified antibodies of the invention can efficiently transduce TPO signal into cells. The pharmaceutical preparations containing them are useful for treating platelet-reduction-related blood diseases and thrombocytopenia caused by chemotherapy for cancers or leukemia. It is further expected that the antibody of the invention can be used as a contrast agent by RI-labeling. The effect can be enhanced by attaching to a RI-compound or a toxin.

## BEST MODE FOR WORKING THE INVENTION

[0077] The present invention will concretely be illustrated in reference to the following examples, which in no way limit the scope of the invention.

[0078] For illustrating the production process of the modified antibodies of the invention, examples of producing single chain Fvs are shown below. Mouse antibodies against human IAP, MABL-1 and MABL-2 were used in the examples of producing the modified antibodies. Hybridomas MABL-1 and MABL-2 producing them respectively were internationally deposited as FERM BP-6100 and FERM BP-6101 with the National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology, Minister of International Trade and Industry (1-3 Higasi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan), an authorized depository for microorganisms, on September 11, 1997.

## Examples

Example 1 (Cloning of DNAs encoding V region of mouse monoclonal antibodies to human IAP)

[0079] DNAs encoding variable regions of the mouse monoclonal antibodies to human IAP, MABL-1 and MABL-2, were cloned as follows.

### 1.1 Preparation of messenger RNA (mRNA)

[0080] mRNAs of the hybridomas MABL-1 and MABL-2 were obtained by using mRNA Purification Kit (Pharmacia Biotech).

### 1.2 Synthesis of double-stranded cDNA

[0081] Double-stranded cDNA was synthesized from about 1 µg of the mRNA using Marathon cDNA Amplification Kit (CLONTECH) and an adapter was linked thereto.

### 1.3 PCR Amplification of genes encoding variable regions of an antibody by

[0082] PCR was carried out using Thermal Cycler (PERKIN ELMER).

(1) Amplification of a gene coding for L chain V region of MABL-1

**[0083]** Primers used for the PCR method are Adapter Primer-1 (CLONTECH) shown in SEQ ID No. 1, which hybridizes to a partial sequence of the adapter, and MKC (Mouse Kappa Constant) primer (Bio/Technology, 9, 88-89, 1991) shown in SEQ ID No. 2, which hybridizes to the mouse kappa type L

chain V region.

**[0084]** 50 µl of the PCR solution contains 5 µl of 10 x PCR Buffer II, 2 mM MgCl<sub>2</sub>, 0.16 mM dNTPs (dATP, dGTP, dCTP and dTTP), 2.5 units of a DNA polymerase, AmpliTaq Gold (PERKIN ELMER), 0.2 µM of the adapter primer of SEQ ID No. 1, 0.2 µM of the MKC primer of SEQ ID No. 2 and 0.1 µg of the double-stranded cDNA derived from MABL-1. The solution was preheated at 94°C of the initial temperature for 9 minutes and then heated at 94°C for 1 minute, at 60°C for 1 minute and at 72°C for 1 minute 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72°C for 10 minutes.

(2) Amplification of cDNA encoding H chain V region of MABL-1

**[0085]** The Adapter Primer-1 shown in SEQ ID No. 1 and MHC-γ1 (Mouse Heavy Constant) primer (Bio/Technology, 9, 88-89, 1991) shown in SEQ ID No. 3 were used as primers for PCR.

**[0086]** The amplification of cDNA was performed according to the method of the amplification of the L chain V region gene, which was described in Example 1.3-(1), except for using 0.2 µM of the MHC-γ1 primer instead of 0.2 µM of the MKC primer.

(3) Amplification of cDNA encoding L chain V region of MABL-2

**[0087]** The Adapter Primer-1 of SEQ ID No. 1 and the MKC primer of SEQ ID No. 2 were used as primers for PCR.

**[0088]** The amplification of cDNA was carried out according to the method of the amplification of the L chain V region gene of MABL-1 which was described in Example 1.3-(1), except for using 0.1 µg of the double-stranded cDNA derived from MABL-2 instead of 0.1 µg of the double-stranded cDNA from MABL-1.

(4) Amplification of cDNA encoding H chain V region of MABL-2

**[0089]** The Adapter Primer-1 of SEQ ID No. 1 and MHC-γ2a primer (Bio/Technology, 9, 88-89, 1991) shown in SEQ ID No. 4 were used as primers for PCR.

**[0090]** The amplification of cDNA was performed according to the method of the amplification of the L chain V region gene, which was described in Example 1.3-(3), except for using 0.2 µM of the MHC-γ2a primer instead of 0.2 µM of the MKC primer.

1.4 Purification of PCR products

**[0091]** The DNA fragment amplified by PCR as described above was purified using the QIAquick PCR Purification Kit (QIAGEN) and dissolved in 10 mM Tris-HCl (pH 8.0) containing 1 mM EDTA.

1.5 Ligation and Transformation

**[0092]** About 140 ng of the DNA fragment comprising the gene encoding the mouse kappa type L chain V region derived from MABL-1 as prepared above was ligated with 50 ng of pGEM-T Easy vector (Promega) in the reaction buffer comprising 30 mM Tris-HCl (pH 7.8), 10 mM MgCl<sub>2</sub>, 10 mM dithiothreitol, 1 mM ATP and 3 units of T4 DNA Ligase (Promega) at 15°C for 3 hours.

**[0093]** Then, 1 µl of the reaction mixture was added to 50 µl of *E. coli* DH5α competent cells (Toyobo Inc.) and the cells were stored on ice for 30 minutes, incubated at 42°C for 1 minute and stored on ice for 2 minutes again. 100 µl of SOC medium (GIBCO BRL) was added. The cells of *E. coli* were plated on LB (Molecular Cloning: A Laboratory Manual, Sambrook et al., Cold Spring Harbor Laboratory Press, 1989) agar medium containing 100 µg/ml of ampicillin (SIGMA) and cultured at 37°C overnight to obtain the transformant of *E. coli*.

**[0094]** The transformant was cultured in 3 ml of LB medium containing 50 µg/ml of ampicillin at 37°C overnight and the plasmid DNA was prepared from the culture using the QIAprep Spin Miniprep Kit (QIAGEN).

**[0095]** The resulting plasmid comprising the gene encoding the mouse kappa type L chain V region derived from the hybridoma MABL-1 was designated as pGEM-M1L.

**[0096]** According to the same manner as described above, a plasmid comprising the gene encoding the mouse H chain V region derived from the hybridoma MABL-1 was prepared from the purified DNA fragment and designated as pGEM-M1H.

**[0097]** A plasmid comprising the gene encoding the mouse kappa type L chain V region derived from the hybridoma MABL-2 was prepared from the purified DNA fragment and designated as pGEM-M2L.

**[0098]** A plasmid comprising the gene encoding the mouse H chain V region derived from the hybridoma MABL-2 was prepared from the purified DNA fragment and designated as pGEM-M2H.

#### Example 2 (DNA Sequencing)

**[0099]** The nucleotide sequence of the cDNA encoding region in the aforementioned plasmids was determined using Auto DNA Sequencer (Applied Biosystem) and ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystem) according to the manufacturer's protocol.

**[0100]** The nucleotide sequence of the gene encoding the L chain V region from the mouse antibody MABL-1, which is included in the plasmid pGEM-M1L, is shown in SEQ ID No. 5.

**[0101]** The nucleotide sequence of the gene encoding the H chain V region from the mouse antibody MABL-1, which is included in the plasmid pGEM-M1H is shown in SEQ ID No. 6.

**[0102]** The nucleotide sequence of the gene encoding the L chain V region from the mouse antibody MABL-2, which is included in the plasmid pGEM-M2L, is shown in SEQ ID No. 7.

**[0103]** The nucleotide sequence of the gene encoding the H chain V region from the mouse antibody MABL-2, which is included in the plasmid pGEM-M2H, is shown in SEQ ID No. 8.

#### Example 3 (Determination of CDR)

**[0104]** The V regions of L chain and H chain generally have a similarity in their structures and each four framework regions therein are linked by three hypervariable regions, i.e., complementarity determining regions (CDR). An amino acid sequence of the framework is relatively well conserved, while an amino acid sequence of CDR has extremely high variation (Kabat, E.A., et al., "Sequences of Proteins of Immunological Interest", US Dept. Health and Human Services, 1983).

**[0105]** On the basis of these facts, the amino acid sequences of the variable regions from the mouse monoclonal antibodies to human IAP were applied to the database of amino acid sequences of the antibodies made by Kabat et al. to investigate the homology. The CDR regions were determined based on the homology as shown in Table 1.

Table 1

| Plasmid  | SEQ ID No. | CDR(1) | CDR(2) | CDR(3)  |
|----------|------------|--------|--------|---------|
| pGEM-M1L | 5          | 43-58  | 74-80  | 113-121 |
| pGEM-M1H | 6          | 50-54  | 69-85  | 118-125 |
| pGEM-M2L | 7          | 43-58  | 74-80  | 113-121 |
| pGEM-M2H | 8          | 50-54  | 69-85  | 118-125 |

#### Example 4 (Identification of Cloned cDNA Expression)

(Preparation of Chimera MABL-1 antibody and Chimera MABL-2 antibody.)

##### 4.1 Preparation of vectors expressing chimera MABL-1 antibody

**[0106]** cDNA clones, pGEM-M1L and pGEM-M1H, encoding the V regions of the L chain and the H chain of the mouse antibody MABL-1, respectively, were modified by the PCR method and introduced into the HEF expression vector (W092/19759) to prepare vectors expressing chimera MABL-1 antibody.

**[0107]** A forward primer MLS (SEQ ID No. 9) for the L chain V region and a forward primer MHS (SEQ ID No. 10) for the H chain V region were designed to hybridize to a DNA encoding the beginning of the leader sequence of each V region and to contain the Kozak consensus sequence (J. Mol. Biol., 196, 947-950, 1987) and HindIII restriction enzyme site. A reverse primer MLAS (SEQ ID No. 11) for the L chain V region and a reverse primer MHAS (SEQ ID No. 12) for the H chain V region were designed to hybridize to a DNA encoding the end of the J region and to contain the splice donor sequence and BamHI restriction enzyme site.

**[0108]** 100  $\mu$ l of a PCR solution comprising 10  $\mu$ l of  $10 \times$  PCR Buffer II, 2 mM  $MgCl_2$ , 0.16 mM dNTPs (dATP, dGTP,

dCTP and dTTP), 5 units of DNA polymerase AmpliTaq Gold, 0.4  $\mu$ M each of primers and 8 ng of the template DNA (pGEM-M1L or pGEM-M1H was preheated at 94°C of the initial temperature for 9 minutes and then heated at 94°C for 1 minute, at 60°C for 1 minute and at 72°C for 1 minute 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72°C for 10 minutes.

[0109] The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and then digested with HindIII and BamHI. The product from the L chain V region was cloned into the HEF expression vector, HEF-K and the product from the H chain V region was cloned into the HEF expression vector, HEF- $\gamma$ . After DNA sequencing, plasmids containing a DNA fragment with a correct DNA sequence are designated as HEF-M1L and HEF-M1H, respectively.

#### 4.2 Preparation of vectors expressing chimera MABL-2 antibodies

[0110] Modification and cloning of cDNA were performed in the same manner described in Example 4.1 except for using pGEM-M2L and pGEM-M2H as template DNA instead of pGEM-M1L and pGEM-M1H. After DNA sequencing, plasmids containing DNA fragments with correct DNA sequences are designated as HEF-M2L and HEF-M2H, respectively.

#### 4.3 Transfection to COS7 cells

[0111] The aforementioned expression vectors were tested in COS7 cells to observe the transient expression of the chimera MABL-1 and MABL-2 antibodies.

##### (1) Transfection with genes for the chimera MABL-1 antibody

[0112] COS7 cells were co-transformed with the HEF-M1L and HEF-M1H vectors by electroporation using the Gene Pulser apparatus (BioRad). Each DNA (10  $\mu$ g) and 0.8 ml of PBS with  $1 \times 10^7$  cells/ml were added to a cuvette. The mixture was treated with pulse at 1.5 kV, 25  $\mu$ F of electric capacity.

[0113] After the restoration for 10 minutes at a room temperature, the electroporated cells were transferred into DMEM culture medium (GIBCO BRL) containing 10%  $\gamma$ -globulin-free fetal bovine serum. After culturing for 72 hours, the supernatant was collected, centrifuged to remove cell fragments and recovered.

##### (2) Transfection with genes coding for the chimera MABL-2 antibody

[0114] The co-transfection to COS7 cells with the genes coding for the chimera MABL-2 antibody was carried out in the same manner as described in Example 4.3-(1) except for using the HEF-M2L and HEF-M2H vectors instead of the HEF-M1L and HEF-M1H vectors. The supernatant was recovered in the same manner.

#### 4.4 Flow cytometry

[0115] Flow cytometry was performed using the aforementioned culture supernatant of COS7 cells to measure binding to the antigen. The culture supernatant of the COS7 cells expressing the chimera MABL-1 antibody or the COS7 cells expressing the chimera MABL-2 antibody, or human IgG antibody (SIGMA) as a control was added to  $4 \times 10^5$  cells of mouse leukemia cell line L1210 expressing human IAP and incubated on ice. After washing, the FITC-labeled anti-human IgG antibody (Cappel) was added thereto. After incubating and washing, the fluorescence intensity thereof was measured using the FACScan apparatus (BECTON DICKINSON).

[0116] Since the chimera MABL-1 and MABL-2 antibodies were specifically bound to L1210 cells expressing human IAP, it is confirmed that these chimera antibodies have proper structures of the V regions of the mouse monoclonal antibodies MABL-1 and MABL-2, respectively (Figs. 1-3).

#### Example 5 (Preparation of reconstructed Single chain Fv (scFv) of the antibody MABL-1 and antibody MABL-2)

##### 5.1 Preparation of reconstructed single chain Fv of antibody MABL-1

[0117] The reconstructed single chain Fv of antibody MABL-1 was prepared as follows. The H chain V region and the L chain V of antibody MABL-1, and a linker were respectively amplified by the PCR method and were connected to produce the reconstructed single chain Fv of antibody MABL-1. The production method is illustrated in Fig. 4. Six primers (A-F) were employed for the production of the single chain Fv of antibody MABL-1. Primers A, C and E have a sense sequence and primers B, D and F have an antisense sequence.

[0118] The forward primer VHS for the H chain V region (Primer A, SEQ ID No. 13) was designed to hybridize to a

DNA encoding the N-terminal of the H chain V region and to contain NcoI restriction enzyme recognition site. The reverse primer VHAS for H chain V region (Primer B, SEQ ID No. 14) was designed to hybridize to a DNA coding the C-terminal of the H chain V region and to overlap with the linker.

[0119] The forward primer LS for the linker (Primer C, SEQ ID No. 15) was designed to hybridize to a DNA encoding the N-terminal of the linker and to overlap with a DNA encoding the C-terminal of the H chain V region. The reverse primer LAS for the linker (Primer D, SEQ ID No. 16) was designed to hybridize to a DNA encoding the C-terminal of the linker and to overlap with a DNA encoding the N-terminal of the L chain V region.

[0120] The forward primer VLS for the L chain V region (Primer E, SEQ ID No. 17) was designed to hybridize to a DNA encoding the C-terminal of the linker and to overlap with a DNA encoding the N-terminal of the L chain V region. The reverse primer VLAS-FLAG for L chain V region (Primer F, SEQ ID No. 18) was designed to hybridize to a DNA encoding the C-terminal of the L chain V region and to have a sequence encoding the FLAG peptide (Hopp, T. P. et al., *Bio/Technology*, 6, 1204-1210, 1988), two stop codons and EcoRI restriction enzyme recognition site.

[0121] In the first PCR step, three reactions, A-B, C-D and E-F, were carried out and PCR products thereof were purified. Three PCR products obtained from the first PCR step were assembled by their complementarity. Then, the primers A and F were added and the full length DNA encoding the reconstructed single chain Fv of antibody MABL-1 was amplified (Second PCR). In the first PCR, the plasmid pGEM-M1H encoding the H chain V region of antibody MABL-1 (see Example 2), a plasmid pSC-DP1 which comprises a DNA sequence encoding a linker region comprising: Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser (SEQ ID No. 19) (Huston, J.S., et al., *Proc. Natl. Acad. Sci. USA*, 85, 5879-5883, 1988) and the plasmid pGEM-M1L encoding the L chain V region of antibody MABL-1 (see Example 2) were employed as template, respectively.

[0122] 50 µl of the solution for the first PCR step comprises 5 µl of 10 × PCR Buffer II, 2 mM MgCl<sub>2</sub>, 0.16 mM dNTPs, 2.5 units of DNA polymerase, AmpliTaq Gold (PERKIN ELMER), 0.4 µM each of primers and 5 ng each of template DNA. The PCR solution was preheated at 94°C of the initial temperature for 9 minutes and then heated at 94°C for 1 minute, at 65°C for 1 minute and at 72°C for 1 minute and 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72°C for 7 minutes.

[0123] The PCR products A-B (371bp), C-D (63bp) and E-F (384bp) were purified using the QIAquick PCR Purification Kit (QIAGEN) and were assembled in the second PCR. In the second PCR, 98 µl of a PCR solution comprising 120 ng of the first PCR product A-B, 20 ng of the PCR product C-D and 120 ng of the PCR product E-F, 10 µl of 10 × PCR Buffer II, 2mM MgCl<sub>2</sub>, 0.16 mM dNTPs, 5 units of DNA polymerase AmpliTaq Gold (PERKIN ELMER) was preheated at 94°C of the initial temperature for 8 minutes and then heated at 94°C for 2 minutes, at 65°C for 2 minutes and at 72°C for 2 minutes in order. This temperature cycle was repeated twice and then 0.4 µM each of primers A and F were added into the reaction, respectively. The mixture was preheated at 94°C of the initial temperature for 1 minutes and then heated at 94°C for 1 minute, at 65°C for 1 minute and at 72°C for 1 minute and 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72°C for 7 minutes.

[0124] A DNA fragment of 843 bp produced by the second PCR was purified and digested by NcoI and EcoRI. The resultant DNA fragment was cloned into pSCFVT7 vector. The expression vector pSCFVT7 contains a pelB signal sequence suitable for *E. coli* periplasmic expression system (Lei, S.P., et al., *J. Bacteriology*, 169, 4379-4383, 1987). After the DNA sequencing, the plasmid containing the DNA fragment encoding correct amino acid sequence of the reconstructed single chain Fv of antibody MABL-1 is designated as "pscM1" (see Fig. 5). The nucleotide sequence and the amino acid sequence of the reconstructed single chain Fv of antibody MABL-1 contained in the plasmid pscM1 are shown in SEQ ID No. 20.

[0125] The pscM1 vector was modified by the PCR method to prepare a vector expressing the reconstructed single chain Fv of antibody MABL-1 in mammalian cells. The resultant DNA fragment was introduced into pCHO1 expression vector. This expression vector, pCHO1, was constructed by digesting DHFR-ΔE-rvH-PM1-f (W092/19759) with EcoRI and SmaI to eliminate the antibody gene and connecting the EcoRI-NotI-BamHI Adapter (Takara Shuzo) thereto.

[0126] As a forward primer for PCR, Sal-VHS primer shown in SEQ ID No. 21 was designed to hybridize to a DNA encoding the N-terminal of the H chain V region and to contain Sall restriction enzyme recognition site. As a reverse primer for PCR, FRHlanti primer shown in SEQ ID No. 22 was designed to hybridize to a DNA encoding the end of the first framework sequence.

[0127] 100 µl of PCR solution comprising 10 µl of 10 × PCR Buffer II, 2 mM MgCl<sub>2</sub>, 0.16 mM dNTPs, 5 units of the DNA polymerase, AmpliTaq Gold, 0.4 µl M each of primer and 8 ng of the template DNA (pscM1) was preheated at 95°C of the initial temperature for 9 minutes and then heated at 95°C for 1 minute, at 60°C for 1 minute and at 72°C for 1 minute and 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72°C for 7 minutes.

[0128] The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and digested by Sall and MboII to obtain a DNA fragment encoding the N-terminal of the reconstructed single chain Fv of antibody MABL-1. The pscM1 vector was digested by MboII and EcoRI to obtain a DNA fragment encoding the C-terminal of the reconstructed single chain Fv of antibody MABL-1. The Sall-MboII DNA fragment and the MboII-EcoRI DNA fragment were cloned

into pCHO1-Igs vector. After DNA sequencing, the plasmid comprising the desired DNA sequence was designated as "pCHOM1" (see Fig. 6). The expression vector, pCHO1-Igs, contains a mouse IgG1 signal sequence suitable for the secretion-expression system in mammalian cells (Nature, 322, 323-327, 1988). The nucleotide sequence and the amino acid sequence of the reconstructed single chain Fv of antibody MABL-1 contained in the plasmid pCHOM1 are shown in SEQ ID No. 23.

## 5.2 Preparation of reconstructed single chain Fv of antibody MABL-2

**[0129]** The reconstructed single chain Fv of antibody MABL-2 was prepared in accordance with the aforementioned Example 5.1. Employed in the first PCR step were plasmid pGEM-M2H encoding the H chain V region of MABL-2 (see Example 2) instead of pGEM-M1H and plasmid pGEM-M2L encoding the L chain V region of MABL-2 (see Example 2) instead of pGEM-M1L, to obtain a plasmid pscM2 which comprises a DNA fragment encoding the desired amino acid sequence of the single chain Fv of antibody MABL-2. The nucleotide sequence and the amino acid sequence of the reconstructed single chain Fv of antibody MABL-2 contained in the plasmid pscM2 are shown in SEQ ID No. 24.

**[0130]** The pscM2 vector was modified by the PCR method to prepare a vector, pCHOM2, for the expression in mammalian cells which contains the DNA fragment encoding the correct amino acid sequence of reconstructed the single chain Fv. of antibody MABL-2. The nucleotide sequence and the amino acid sequence of the reconstructed single chain Fv of antibody MABL-2 contained in the plasmid pCHOM2 are shown in SEQ ID No. 25.

## 5.3 Transfection to COS7 cells

**[0131]** The pCHOM2 vector was tested in COS7 cells to observe the transient expression of the reconstructed single chain Fv of antibody MABL-2.

**[0132]** The COS7 cells were transformed with the pCHOM2 vector by electroporation using the Gene Pulser apparatus (BioRad). The DNA (10 µg) and 0.8 ml of PBS with  $1 \times 10^7$  cells/ml were added to a cuvette. The mixture was treated with pulse at 1.5 kV, 25 µF of electric capacity.

**[0133]** After the restoration for 10 minutes at a room temperature, the electroporated cells were transferred into IMDM culture medium (GIBCO BRL) containing 10% fetal bovine serum. After culturing for 72 hours, the supernatant was collected, centrifuged to remove cell fragments and recovered.

## 5.4 Detection of the reconstructed single chain Fv of antibody MABL-2 in culture supernatant of COS7 cells

**[0134]** The existence of the single chain Fv of antibody MABL-2 in the culture supernatant of COS7 cells which had been transfected with the pCHOM2 vector was confirmed by the Western Blotting method.

**[0135]** The culture supernatant of COS7 cells transfected with the pCHOM2 vector and the culture supernatant of COS7 cells transfected with the pCHO1 as a control were subjected to SDS electrophoresis and transferred to REINFORCED NC membrane (Schleicher & Schuell). The membrane was blocked with 5% skim milk (Morinaga Nyu-gyo), washed with 0.05% Tween 20-PBS and mixed with an anti-FLAG antibody (SIGMA). The membrane was incubated at room temperature, washed and mixed with alkaline phosphatase-conjugated mouse IgG antibody (Zymed). After incubating and washing at room temperature, the substrate solution (Kirkegaard Perry Laboratories) was added to develop color (Fig. 7).

**[0136]** A FLAG-peptide-specific protein was detected only in the culture supernatant of the pCHOM2 vector-introduced COS7 cells and thus it is confirmed that the reconstructed single chain Fv of antibody MABL-2 was secreted in this culture supernatant.

## 5.5 Flow cytometry

**[0137]** Flow cytometry was performed using the aforementioned COS7 cells culture supernatant to measure the binding to the antigen. The culture supernatant of the COS7 cells expressing the reconstructed single chain Fv of antibody MABL-2 or the culture supernatant of COS7 cells transformed with pCHO1 vector as a control was added to  $2 \times 10^5$  cells of the mouse leukemia cell line L1210 expressing human Integrin Associated Protein (IAP) or the cell line L1210 transformed with pCOS1 as a control. After incubating on ice and washing, the mouse anti-FLAG antibody (SIGMA) was added. Then the cells were incubated and washed. Then, the FITC labeled anti-mouse IgG antibody (BECTON DICKINSON) was added thereto and the cells were incubated and washed again. Subsequently, the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON).

**[0138]** Since the single chain Fv of antibody MABL-2 was specifically bound to L1210 cells expressing human IAP, it is confirmed that the reconstructed single chain Fv of antibody MABL-2 has an affinity to human Integrin Associated Protein (IAP) (see Figs. 8-11).

## 5.6 Competitive ELISA

**[0139]** The binding activity of the reconstructed single chain Fv of antibody MABL-2 was measured based on the inhibiting activity against the binding of mouse monoclonal antibodies to the antigen.

**[0140]** The anti-FLAG antibody adjusted to 1 µg/ml was added to each well on 96-well plate and incubated at 37°C for 2 hours. After washing, blocking was performed with 1% BSA-PBS. After incubating and washing at a room temperature, the culture supernatant of COS7 cells into which the secretion-type human IAP antigen gene (SEQ ID No. 26) had been introduced was diluted with PBS into twofold volume and added to each well. After incubating and washing at a room temperature, a mixture of 50 µl of the biotinized MABL-2 antibody adjusted to 100 ng/ml and 50 µl of sequentially diluted supernatant of the COS7 cells expressing the reconstructed single chain Fv of antibody MABL-2 were added into each well. After incubating and washing at a room temperature, the alkaline phosphatase-conjugated streptavidin (Zymed) was added into each well. After incubating and washing at a room temperature, the substrate solution (SIGMA) was added and absorbance of the reaction mixture in each well was measured at 405 nm.

**[0141]** The results revealed that the reconstructed single chain Fv of antibody MABL-2 (MABL2-scFv) evidently inhibited concentration-dependently the binding of the mouse antibody MABL-2 to human IAP antigen in comparison with the culture supernatant of the PCHO1-introduced COS7 cells as a control (Fig. 12). Accordingly, it is suggested that the reconstructed single chain Fv of antibody MABL-2 has the correct structure of each of the V regions from the mouse monoclonal antibody MABL-2.

## 5.7 Apoptosis-inducing Effect in vitro

**[0142]** An apoptosis-inducing action of the reconstructed single chain Fv of antibody MABL-2 was examined by Annexin-V staining (Boehringer Mannheim) using the L1210 cells transfected with human IAP gene, the L1210 cells transfected with the pCOS1 vector as a control and CCRF-CEM cells.

**[0143]** To each  $1 \times 10^5$  cells of the above cells was added the culture supernatant of the COS7 cells expressing the reconstructed single chain Fv of antibody MABL-2 or the culture supernatant of COS7 cells transfected with the pCHO1 vector as a control at 50% final concentration and the mixtures were cultured for 24 hours. Then, the Annexin-V staining was performed and the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON).

**[0144]** Results of the Annexin-V staining are shown in Figs. 13-18, respectively. Dots in the left-lower region represent living cells and dots in the right-lower region represent cells at the early stage of apoptosis and dots in the right-upper region represent cells at the late stage of apoptosis. The results show that the reconstructed single chain Fv of antibody MABL-2 (MABL2-scFv) remarkably induced cell death of L1210 cells specific to human IAP antigen (Figs. 13-16) and that the reconstructed single chain Fv also induced remarkable cell death of CCRF-CEM cells in comparison with the control (Figs. 17-18).

## 5.8 Expression of MABL-2 derived single chain Fv in CHO cells

**[0145]** CHO cells were transfected with the pCHOM2 vector to establish a CHO cell line which constantly expresses the single chain Fv (polypeptide) derived from the antibody MABL-2.

**[0146]** CHO cells were transformed with the pCHOM2 vector by the electroporation using the Gene Pulser apparatus (BioRad). A mixture of DNA (10 µg) and 0.7 ml of PBS with CHO cells ( $1 \times 10^7$  cells/ml) was added to a cuvette. The mixture was treated with pulse at 1.5 kV, 25 µF of electric capacity. After the restoration for 10 minutes at a room temperature, the electroporated cells were transferred into nucleic acid free α-MEM medium (GIBCO BRL) containing 10% fetal bovine serum and cultured. The expression of desired protein in the resultant clones was confirmed by SDS-PAGE and a clone with a high expression level was selected as a cell line producing the single chain Fv derived from the antibody MABL-2. The cell line was cultured in serum-free medium CHO-S-SFM II (GIBCO BRL) containing 10 nM methotrexate (SIGMA). Then, the culture supernatant was collected, centrifuged to remove cell fragments and recovered.

## 5.9 Purification of MABL-2 derived single chain Fv produced in CHO cells

**[0147]** The culture supernatant of the CHO cell line expressing the single chain Fv obtained in Example 5.8 was concentrated up to twenty times using a cartridge for the artificial dialysis (PAN130SF, ASAHI MEDICALS). The concentrated solution was stored at -20°C and thawed on purification.

**[0148]** Purification of the single chain Fv from the culture supernatant of the CHO cells was performed using three kinds of chromatography, i.e., Blue-sepharose, a hydroxyapatite and a gel filtration.

(1) Blue-sepharose column chromatography

**[0149]** The concentrated supernatant was diluted to ten times with 20 mM acetate buffer (pH 6.0) and centrifuged to remove insoluble materials (10000 × rpm, 30 minutes). The supernatant was applied onto a Blue-sepharose column (20 ml) equilibrated with the same buffer. After washing the column with the same buffer, proteins adsorbed in the column were eluted by a stepwise gradient of NaCl in the same buffer, 0.1, 0.2, 0.3, 0.5 and up to 1.0 M. The pass-through fraction and each eluted fraction were analyzed by SDS-PAGE. The fractions in which the single chain Fv were confirmed (the fractions eluted at 0.1 to 0.3M NaCl) were pooled and concentrated up to approximately 20 times using CentriPrep-10 (AMICON).

(2) Hydroxyapatite

**[0150]** The concentrated solution obtained in (1) was diluted to 10 times with 10 mM phosphate buffer (pH 7.0) and applied onto the hydroxyapatite column (20 ml, BIORAD). The column was washed with 60 ml of 10 mM phosphate buffer (pH 7.0). Then, proteins adsorbed in the column were eluted by a linear gradient of sodium phosphate buffer up to 200 mM (see Fig. 19). The analysis of each fraction by SDS-PAGE confirmed the single chain Fv in fraction A and fraction B.

(3) Gel filtration

**[0151]** Each of fractions A and B in (2) was separately concentrated with CentriPrep-10 and applied onto TSKgel G3000SWG column (21.5 x 600 mm) equilibrated with 20 mM acetate buffer (pH 6.0) containing 0.15 M NaCl. Chromatograms are shown in Fig. 20. The analysis of the fractions by SDS-PAGE confirmed that both major peaks (AI and BI) are of desired single chain Fv. In the gel filtration analysis, the fraction A was eluted at 36 kDa of apparent molecular weight and the fraction B was eluted at 76 kDa. The purified single chain Fvs (AI, BI) were analyzed with 15% SDS polyacrylamide gel. Samples were treated in the absence or presence of a reductant and the electrophoresis was carried out in accordance with the Laemmli's method. Then the protein was stained with Coomassie Brilliant Blue. As shown in Fig. 21, both AI and BI gave a single band at 35 kDa of apparent molecular weight, regardless of the absence or presence of the reductant. From the above, it is concluded that AI is a monomer of the single chain Fv and BI is a non-covalently bound dimer of the single chain Fv. The gel filtration analysis of the fractions AI and BI with TSKgel G3000SW column (7.5 × 60 mm) revealed that a peak of the monomer is detected only in the fraction AI and a peak of the dimer is detected only in the fraction BI (Fig. 22). The dimer fraction (fraction BI) accounted for 4 period of total single chain Fvs. More than 90% of the dimer in the dimer fraction was stably preserved for more than a month at 4°C.

5.10 Construction of vector expressing single chain Fv derived from antibody MABL-2 in E. coli cell

**[0152]** The pscM2 vector was modified by the PCR method to prepare a vector effectively expressing the single chain Fv from the antibody MABL-2 in *E. coli* cells. The resultant DNA fragment was introduced into pSCFVT7 expression vector.

**[0153]** As a forward primer for PCR, Nde-VHSm02 primer shown in SEQ ID No. 27 was designed to hybridize to a DNA encoding the N-terminal of the H chain V region and to contain a start codon and NdeI restriction enzyme recognition site. As a reverse primer for PCR, VLAS primer shown in SEQ ID No. 28 was designed to hybridize to a DNA encoding the C-terminal of the L chain V region and to contain two stop codons and EcoRI restriction enzyme recognition site. The forward primer, Nde-VHSm02, comprises five point mutations in the part hybridizing to the DNA encoding the N-terminal of the H chain V region for the effective expression in *E. coli*.

**[0154]** 100 µl of a PCR solution comprising 10 µl of 10 x PCR Buffer #1, 1 mM MgCl<sub>2</sub>, 0.2 mM dNTPs, 5 units of KOD DNA polymerase (all from TOYOBO), 1 µM of each primer and 100 ng of a template DNA (pscM2) was heated at 98°C for 15 seconds, at 65°C for 2 seconds and at 74°C for 30 seconds in order. This temperature cycle was repeated 25 times.

**[0155]** The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and digested by NdeI and EcoRI, and then the resulting DNA fragment was cloned into pSCFVT7 vector, from which pelB signal sequence had been eliminated by the digestion with NdeI and EcoRI. After DNA sequencing, the resulting plasmid comprising a DNA fragment with the desired DNA sequence is designated as "pscM2DEm02" (see Fig. 23). The nucleotide sequence and the amino acid sequence of the single chain Fv derived from the antibody MABL-2 contained in the plasmid pscM2DEm02 are shown in SEQ ID No. 29.

### 5.11 Expression of single chain Fv derived from antibody MABL-2 in *E. coli* cells

**[0156]** *E. coli* BL21(DE3)pLysS (STRATAGENE) was transformed with pscM2DEm02 vector to obtain a strain of *E. coli* expressing the single chain Fv derived from antibody MABL-2. The resulting clones were examined for the expression of the desired protein using SDS-PAGE, and a clone with a high expression level was selected as a strain producing the single chain Fv derived from antibody MABL-2.

### 5.12 Purification of single chain Fv derived from antibody MABL-2 produced in *E. coli*

**[0157]** A single colony of *E. coli* obtained by the transformation was cultured in 3 ml of LB medium at 28°C for 7 hours and then in 70 ml of LB medium at 28°C overnight. This pre-culture was transplanted to 7 L of LB medium and cultured at 28°C with stirring at 300 rpm using the Jar-fermenter. When an absorbance of the medium reached O.D.<sub>550</sub>=1.5, the bacteria were induced with 1 mM IPTG and then cultured for 3 hours.

**[0158]** The culture medium was centrifuged (10000 × g, 10 minutes) and the precipitated bacteria were recovered. To the bacteria was added 50 mM Tris-HCl buffer (pH 8.0) containing 5 mM EDTA, 0.1 M NaCl and 1% Triton X-100 and the bacteria were disrupted by ultrasonication (out put: 4, duty cycle: 70%, 1 minute × 10 times). The suspension of disrupted bacteria was centrifuged (12000 × g, 10 minutes) to precipitate inclusion body. Isolated inclusion body was mixed with 50 mM Tris-HCl buffer (pH 8.0) containing 5 mM EDTA, 0.1 M NaCl and 4% Triton X-100, treated by ultrasonication (out put: 4, duty cycle: 50%, 30 seconds × 2 times) again and centrifuged (12000 × g, 10 minutes) to isolate the desired protein as precipitate and to remove containment proteins included in the supernatant.

**[0159]** The inclusion body comprising the desired protein was lysed in 50 mM Tris-HCl buffer (pH 8.0) containing 6 M Urea, 5 mM EDTA and 0.1 M NaCl and applied onto Sephacryl S-3,00 gel filtration column (5 × 90 cm, Amersham Pharmacia) equilibrated with 50 mM Tris-HCl buffer (pH 8.0) containing 4M Urea, 5 mM EDTA, 0.1 M NaCl and 10 mM mercaptoethanol at a flow rate of 5 ml/minutes to remove associated single chain Fvs with high-molecular weight. The obtained fractions were analyzed with SDS-PAGE and the fractions with high purity of the protein were diluted with the buffer used in the gel filtration up to O.D.<sub>280</sub>=0.25. Then, the fractions were dialyzed three times against 50 mM Tris-HCl buffer (pH 8.0) containing 5 mM EDTA, 0.1 M NaCl, 0.5 M Arg, 2 mM glutathione in the reduced form and 0.2 mM glutathione in the oxidized form in order for the protein to be refolded. Further, the fraction was dialyzed three times against 20 mM acetate buffer (pH 6.0) containing 0.15 M NaCl to exchange the buffer.

**[0160]** The dialysate product was applied onto Superdex 200 pg gel filtration column (2.6 × 60 cm, Amersham Pharmacia) equilibrated with 20 mM acetate buffer (pH 6.0) containing 0.15 M NaCl to remove a small amount of high molecular weight protein which was intermolecularly crosslinked by S-S bonds. As shown in Fig. 24, two peaks, major and sub peaks, were eluted after broad peaks which are expectedly attributed to an aggregate with a high molecular weight. The analysis by SDS-PAGE (see Fig. 21) and the elution positions of the two peaks in the gel filtration analysis suggest that the major peak is of the monomer of the single chain Fv and the sub peak is of the non-covalently bound dimer of the single chain Fv. The non-covalently bound dimer accounted for 4 percent of total single chain Fvs.

### 5.13 Apoptosis-inducing activity in vitro of single chain Fv derived from antibody MABL-2

**[0161]** An apoptosis-inducing action of the single chain Fv from antibody MABL-2 (MABL2-scFv) produced by the CHO cells and *E. coli* was examined according to two protocols by Annexin-V staining (Boehringer Mannheim) using the L1210 cells (hIAP/L1210) into which human IAP gene had been introduced.

**[0162]** In the first protocol sample antibodies at the final concentration of 3 µg/ml were added to 5 × 10<sup>4</sup> cells of hIAP/L1210 cell line and cultured for 24 hours. Sample antibodies, i.e., the monomer and the dimer of the single chain Fv of MABL-2 from the CHO cells obtained in Example 5.9, the monomer and the dimer of the single chain Fv of MABL-2 from *E. coli* obtained in Example 5.12, and the mouse IgG antibody as a control were analyzed. After culturing, the Annexin-V staining was carried out and the fluorescence intensity thereof was measured using the FACScan apparatus (BECTON DICKINSON).

**[0163]** In the second protocol sample antibodies at the final concentration of 3 µg/ml were added to 5 × 10<sup>4</sup> cells of hIAP/L1210 cell line, cultured for 2 hours and mixed with anti-FLAG antibody (SIGMA) at the final concentration of 15 µg/ml and further cultured for 22 hours. Sample antibodies of the monomer of the single chain Fv of MABL-2 from the CHO cells obtained in Example 5.9 and the mouse IgG antibody as a control were analyzed. After culturing, the Annexin-V staining was carried out and the fluorescence intensity thereof was measured using the FACScan apparatus.

**[0164]** Results of the analysis by the Annexin-V staining are shown in Figs. 25-31. The results show that the dimers of the single chain Fv polypeptide of MABL-2 produced in the CHO cells and *E. coli* remarkably induced cell death (Figs. 26, 27) in comparison with the control (Fig. 25), while no apoptosis-inducing action was observed in the monomers of the single chain Fv polypeptide of MABL-2 produced in the CHO cells and *E. coli* (Figs. 28, 29). When anti-FLAG antibody was used together, the monomer of the single chain Fv polypeptide derived from antibody MABL-2 produced

in the CHO cells induced remarkably cell death (Fig. 31) in comparison with the control (Fig. 30).

#### 5.14 Antitumor effect of the monomer and the dimer of scFv/CHO polypeptide with a model mouse of human myeloma

##### (1) Quantitative measurement of human IgG in mouse serum

**[0165]** Measurement of human IgG (M protein) produced by human myeloma cell and contained in mouse serum was carried out by the following ELISA. 100  $\mu$ L of goat anti-human IgG antibody (BIOSOURCE, Lot#7902) diluted to 1  $\mu$ g/mL with 0.1% bicarbonate buffer (pH 9.6) was added to each well on 96 wells plate (Nunc) and incubated at 4°C overnight so that the antibody was immobilized. After blocking, 100  $\mu$ L of the stepwisely diluted mouse serum or human IgG (CAPPEL, Lot#00915) as a standard was added to each well and incubated for 2 hours at a room temperature. After washing, 100  $\mu$ L of alkaline phosphatase-labeled anti-human IgG antibody (BIOSOURCE, Lot#6202) which had been diluted to 5000 times was added, and incubation was carried out for 1 hour at a room temperature. After washing, a substrate solution was added. After incubation, absorbance at 405 nm was measured using the MICROPLATE READER Model 3550 (BioRad). The concentration of human IgG in the mouse serum was calculated based on the calibration curve obtained from the absorbance values of human IgG as the standard.

##### (2) Preparation of antibodies for administration

**[0166]** The monomer and the dimer of the scFv/CHO polypeptide were respectively diluted to 0.4 mg/mL or 0.25 mg/mL with sterile filtered PBS(-) on the day of administration to prepare samples for the administration.

##### (3) Preparation of a mouse model of human myeloma

**[0167]** A mouse model of human myeloma was prepared as follows. KPMM2 cells passaged in vivo (JP-Appl. 7-236475) by SCID mouse (Japan Clare) were suspended in RPMI1640 medium (GIBCO-BRL) containing 10% fetal bovine serum (GIBCO-BRL) and adjusted to  $3 \times 10^7$  cells/mL. 200  $\mu$ L of the KPMM2 cell suspension ( $6 \times 10^6$  cells/mouse) was transplanted to the SCID mouse (male, 6 week-old) via caudal vein thereof, which had been subcutaneously injected with the asialo GM1 antibody (WAKO JUNYAKU, 1 vial dissolved in 5 mL) a day before the transplantation.

##### (4) Administration of antibodies

**[0168]** The samples of the antibodies prepared in (2), the monomer (250  $\mu$ L) and the dimer (400  $\mu$ L), were administered to the model mice of human myeloma prepared in (3) via caudal vein thereof. The administration was started from three days after the transplantation of KPMM2 cells and was carried out twice a day for three days. As a control, 200  $\mu$ L of sterile filtered PBS(-) was likewise administered twice a day for three days via caudal vein. Each group consisted of seven mice.

##### (5) Evaluation of antitumor effect of the monomer and the dimer of scFv/CHO polypeptide with the model mouse of human myeloma

**[0169]** The antitumor effect of the monomer and the dimer of scFv/CHO polypeptide with the model mice of human myeloma was evaluated in terms of the change of human IgG (M protein) concentration in the mouse serum and survival time of the mice. The change of human IgG concentration was determined by measuring it in the mouse serum collected at 24 days after the transplantation of KPMM2 cells by ELISA described in the above (1). The amount of serum human IgG (M protein) in the serum of the PBS(-)-administered group (control) increased to about 8500  $\mu$ g/mL, whereas the amount of human IgG of the scFv/CHO dimer-administered group was remarkably low, that is, as low as one-tenth or less than that of the control group. Thus, the results show that the dimer of scFv/CHO strongly inhibits the growth of the KPMM2 cells (Fig. 32). As shown in Fig. 33, a remarkable elongation of the survival time was observed in the scFv/CHO dimer-administered group in comparison with the PBS(-)-administered group.

**[0170]** From the above, it is confirmed that the dimer of scFv/CHO has an antitumor effect for the human myeloma model mice. It is considered that the antitumor effect of the dimer of scFv/CHO, the modified antibody of the invention, results from the apoptosis-inducing action of the modified antibody.

#### 5.15 Hemagglutination Test

**[0171]** Hemagglutination test and determination of hemagglutination were carried out in accordance with "Immuno-Biochemical Investigation", Zoku-Seikagaku Jikken Koza, edited by the Biochemical Society of Japan, published by

Tokyo Kagaku Dojin.

**[0172]** Blood was taken from a healthy donor using heparin-treated syringes and washed with PBS(-) three times, and then erythrocyte suspension with a final concentration of 2% in PBS(-) was prepared. Test samples were the antibody MABL-2, the monomer and the dimer of the single chain Fv polypeptide produced by the CHO cells, and the monomer and the dimer of the single chain Fv polypeptide produced by *E. coli*, and the control was mouse IgG (ZYMED). For the investigation of the hemagglutination effect, round bottom 96-well plates available from Falcon were used. 50  $\mu$ L per well of the aforementioned antibody samples and 50  $\mu$ L of the 2% erythrocyte suspension were added and mixed in the well. After incubation for 2 hours at 37°C, the reaction mixtures were stored at 4°C overnight and the hemagglutination thereof was determined. As a control, 50  $\mu$ L per well of PBS (-) was used and the hemagglutination test was carried out in the same manner. The mouse IgG and antibody MABL-2 were employed at 0.01, 0.1, 1.0, 10.0 or 100.0  $\mu$ g/mL of the final concentration of the antibodies. The single chain Fvs were employed at 0.004, 0.04, 0.4, 4.0, 40.0 or 80.0  $\mu$ g/mL of the final concentration and further at 160.0  $\mu$ g/mL only in the case of the dimer of the polypeptide produced by *E. coli*. Results are shown in the Table 2. In the case of antibody MABL-2, the hemagglutination was observed at a concentration of more than 0.1  $\mu$ g/mL, whereas no hemagglutination was observed for both the monomer and the dimer of the single chain Fv.

Table 2

| Hemagglutination Test |         |       |      |     |     |     |            |            |            |
|-----------------------|---------|-------|------|-----|-----|-----|------------|------------|------------|
| mIgG                  | Control | 0.01  | 0.1  | 1   | 10  | 100 | $\mu$ g/mL |            |            |
| MABL-2                | -       | -     | -    | -   | -   | -   |            |            |            |
| (intact)              | -       | -     | +    | +++ | +++ | ++  |            |            |            |
| scFv/CHO              | Control | 0.004 | 0.04 | 0.4 | 4   | 40  | 80         | $\mu$ g/mL |            |
| monomer               | -       | -     | -    | -   | -   | -   | -          |            |            |
| scFv/CHO              | -       | -     | -    | -   | -   | -   | -          |            |            |
| dimer                 | -       | -     | -    | -   | -   | -   | -          |            |            |
| scFv/E.coli           | Control | 0.004 | 0.04 | 0.4 | 4   | 40  | 80         | 160        | $\mu$ g/mL |
| monomer               | -       | -     | -    | -   | -   | -   | -          | -          |            |
| scFv/E.coli           | -       | -     | -    | -   | -   | -   | -          | -          |            |
| dimer                 | -       | -     | -    | -   | -   | -   | -          | -          |            |

Example 6 Modified antibody sc(Fv)<sub>2</sub> comprising two H chain V regions and two L chain V regions and antibody MABL-2 scFvs having linkers with different length

#### 6.1 Construction of plasmid expressing antibody MABL-2 sc(Fv)<sub>2</sub>

**[0173]** For the preparation of a plasmid expressing the modified antibody [sc(Fv)<sub>2</sub>] which comprises two H chain V regions and two L chain V regions derived from the antibody MABL-2, the aforementioned pCHOM2, which comprises the DNA encoding scFv derived from the MABL-2 described above, was modified by the PCR method as mentioned below and the resulting DNA fragment was introduced into pCHOM2.

**[0174]** Primers employed for the PCR are EF1 primer (SEQ ID NO: 30) as a sense primer, which is designed to hybridize to a DNA encoding EF1 $\alpha$ , and an antisense primer (SEQ ID NO: 19), which is designed to hybridize to the DNA encoding C-terminal of the L chain V region and to contain a DNA sequence coding for a linker region, and VLLAS primer containing Sall restriction enzyme recognition site (SEQ ID NO 31).

**[0175]** 100  $\mu$ L of the PCR solution comprises 10  $\mu$ L of 10  $\times$  PCR Buffer #1, 1 mM MgCl<sub>2</sub>, 0.2 mM dNTPs (dATP, dGTP, dCTP and dTTP), 5 units of KOD DNA polymerase (Toyobo, Inc.), 1  $\mu$ M of each primer and 100 ng of the template DNA (pCHOM2). The PCR solution was heated at 94°C for 30 seconds, at 50°C for 30 seconds and at 74°C for 1 minute in order. This temperature cycle was repeated 30 times.

**[0176]** The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and digested by Sall. The resultant DNA fragment was cloned into pBluescript KS<sup>+</sup> vector (Toyobo, Inc.). After DNA sequencing, a plasmid comprising the desired DNA sequence was digested by Sall and the obtained DNA fragment was connected using Rapid DNA Ligation Kit(BOEHRINGER MANNHEIM) to pCHOM2 digested by Sall. After DNA sequencing, a plasmid comprising the desired DNA sequence is designated as "pCHOM2(Fv)<sub>2</sub>" (see Fig. 34). The nucleotide sequence and the

amino acid sequence of the antibody MABL-2 sc(Fv)<sub>2</sub> region contained in the plasmid pCHOM2(Fv)<sub>2</sub> are shown in SEQ ID No. 32.

## 6.2 Preparation of Plasmid expressing antibody MABL-2 scFvs having linkers with various length

**[0177]** The scFvs containing linkers with different length and the V regions which are designed in the order of [H chain]-[L chain] (hereinafter "HL") or [L chain]-[H chain] (hereinafter "LH") were prepared using, as a template, cDNAs encoding the H chain and the L chain derived from the MABL-2 as mentioned below.

**[0178]** To construct HL type scFv the PCR procedure was carried out using pCHOM2(Fv)<sub>2</sub> as a template. In the PCR step, a pair of CFHL-F1 primer (SEQ ID NO: 33) and CFHL-R2 primer (SEQ ID NO: 34) or a pair of CFHL-F2 primer (SEQ ID NO: 35) and CFHL-R1 primer (SEQ ID NO: 36) and KOD polymerase were employed. The PCR procedure was carried out by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order to produce a cDNA for the H chain containing a leader sequence at 5'-end or a cDNA for the L chain containing FLAG sequence at 3'-end thereof. The resultant cDNAs for the H chain and the L chain were mixed and PCR was carried out by repeating 5 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order using the mixture as templates and the KOD polymerase. To the reaction mixture were added CFHL-F1 and CFHL-R1 primers and then the PCR reaction was performed by repeating 30 times of the aforementioned temperature cycle to produce a cDNA for HL-0 type without a linker.

**[0179]** To construct LH type scFv, the PCR reaction was carried out using, as a template, pGEM-M2L and pGEM-M2H which contain cDNAs encoding the L chain V region and the H chain V region from the antibody MABL-2, respectively (see JP- Appl. 11-63557). A pair of T7 primer (SEQ ID NO: 37) and CFLH-R2 primer (SEQ ID NO: 38) or a pair of CFLH-F2 primer (SEQ ID NO: 39) and CFLH-R1 (SEQ ID NO: 40) and the KOD polymerase (Toyobo Inc.) were employed. The PCR reaction was performed by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in sequential order to produce a cDNA of an L chain containing a leader sequence at 5'-end or a cDNA of an H chain containing FLAG sequence at 3'-end thereof. The resultant cDNAs of the L chain and the H chain were mixed and PCR was carried out using this mixture as templates and the KOD polymerase by repeating 5 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order. To the reaction mixture were added T7 and CFLH-R1 primers and the reaction was performed by repeating 30 times of the aforementioned temperature cycle. The reaction product was used as a template and PCR was carried out using a pair of CFLH-F4 primer (SEQ ID NO: 41) and CFLH-R1 primer by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order to produce a cDNA of LH-0 type without a linker.

**[0180]** The resultant cDNAs of LH-0 and HL-0 types were digested by EcoRI and BamHI restriction enzymes (Takara Shuzo) and the digested cDNAs were introduced into an expression plasmid INPEP4 for mammalian cells using Ligation High (Toyobo Inc.), respectively. Competent *E. coli* JM109 (Nippon Gene) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using QIAGEN Plasmid Maxi Kit (QIAGEN). Thus plasmids pCF2LH-0 and pCF2HL-0 were prepared.

**[0181]** To construct the expression plasmids of HL type containing linkers with different size, pCF2HL-0, as a template, and CFHL-X3 (SEQ ID NO: 42), CFHL-X4 (SEQ ID NO: 43), CFHL-X5 (SEQ ID NO: 44), CFHL-X6 (SEQ ID NO: 45) or CFHL-X7 (SEQ ID NO: 46), as a sense primer, and BGH-1 (SEQ ID NO: 47) primer, as an antisense primer, which is complementary with the vector sequence were employed. PCR reaction was carried out using the KOD polymerase by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order and the reaction products were digested by restriction enzymes XhoI and BamHI (Takara Shuzo). The digested fragments were introduced between XhoI and BamHI sites in the pCF2HL-0 using Ligation High (Toyobo Inc.), respectively. Competent *E. coli* JM109 was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* by using Qiagen Plasmid Maxi kit. Thus expression plasmids pCF2HL-3, pCF2HL-4, pCF2HL-5, pCF2HL-6 and pCF2HL-7 were prepared.

**[0182]** To construct expression plasmid for the transient expression in COS7 cells the plasmids pCF2HL-0, pCF2HL-3, pCF2HL-4, pCF2HL-5, pCF2HL-6 and pCF2HL-7 were digested by restriction enzymes EcoRI and BamHI (Takara Shuzo) and the resultant fragments of approximately 800 bp were purified with agarose gel electrophoresis. The obtained fragments were introduced between EcoRI and BamHI sites in an expression plasmid pCOS1 for the expression in mammalian cells by using Ligation High (Toyobo Inc.), respectively. Competent *E. coli* DH5α (Toyobo Inc.) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using Qiagen Plasmid Maxi kit. Thus the expression plasmids CF2HL-0/pCOS1, CF2HL-3/pCOS1, CF2HL-4/pCOS1, CF2HL-5/pCOS1, CF2HL-6/pCOS1 and CF2HL-7/pCOS1 were prepared.

**[0183]** As a typical example of these plasmids, the construction of the plasmid CF2HL-0/pCOS1 is illustrated in Fig. 35 and the nucleotide sequence and the amino acid sequence of MABL2-scFv <HL-0> contained in the plasmid are shown in SEQ ID No. 48. Nucleotide sequences and amino acid sequences of the linker regions in these plasmids are

also shown in Fig. 36.

**[0184]** To construct the expression: plasmids of LH type containing linkers with different size, pCF2LH-0, as a template, and CFLH-X3 (SEQ ID NO: 49), CFLH-X4 (SEQ ID NO: 50), CFLH-X5 (SEQ ID NO: 51), CFLH-X6 (SEQ ID NO: 52) or CFLH-X7 (SEQ ID NO: 53), as a sense primer, and BGH-1 primer, as an antisense primer, which is complementary with the vector sequence were employed. PCR reaction was carried out using the KOD polymerase by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order and the reaction products were digested by restriction enzymes XhoI and BamHI. The digested fragments were introduced into the pCF2LH-0 between XhoI and BamHI sites using Ligation High, respectively. Competent *E. coli* DH5 $\alpha$  (Toyobo Inc.) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using Qiagen Plasmid Maxi kit. Thus expression plasmids pCF2LH-3, pCF2LH-4, pCF2LH-5, pCF2LH-6 and pCF2LH-7 were prepared.

**[0185]** To construct expression plasmid for the transient expression in COS7 cells the plasmids pCF2LH-0, pCF2LH-3, pCF2LH-4, pCF2LH-5, pCF2LH-6 and pCF2LH-7 were digested by restriction enzymes EcoRI and BamHI (Takara Shuzo) and the resultant fragments of approximately 800 bp were purified with agarose gel electrophoresis. The obtained fragments were introduced between XhoI and BamHI sites in an expression plasmid pCOS1 for the expression in mammalian cells by using the Ligation High, respectively. Competent *E. coli* DH5 $\alpha$  (Toyobo Inc.) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using the Qiagen Plasmid Maxi kit. Consequently, the expression plasmids CF2LH-0/pCOS1, CF2LH-3/pCOS1, CF2LH-4/pCOS1, CF2LH-5/pCOS1, CF2LH-6/pCOS1 and CF2LH-7/pCOS1 were prepared.

**[0186]** As a typical example of these plasmids, the construction of the plasmid CF2LH-0/pCOS1 is illustrated in Fig. 37 and the nucleotide sequence and the amino acid sequence of MABL2-scFv <LH-0> contained in the plasmid are shown in SEQ ID No. 54. Nucleotide sequences and amino acid sequences of the linker regions in these plasmids are also shown in Fig. 38.

### 6.3 Expression of scFvs and sc(Fv)<sub>2</sub> in COS7 cells

#### (1) Preparation of culture supernatant using serum-containing culture medium

**[0187]** The HL type and LH type of scFvs and sc(Fv)<sub>2</sub> were transiently expressed in COS7 cells (JCRB9127, Japan Health Sciences Foundation). COS7 cells were subcultured in DMEM media (GIBCO BRL) containing 10% fetal bovine serum (HyClone) at 37°C in carbon dioxide atmosphere incubator. The COS7 cells were transfected with CF2HL-0, 3 ~ 7/pCOS1, or CF2LH-0, 3 ~ 7/pCOS1 prepared in Example 6.2 or pCHOM2(Fv)<sub>2</sub> vectors by electroporation using the Gene Pulser apparatus (BioRad). The DNA (10  $\mu$ g) and 0.25 ml of  $2 \times 10^7$  cells/ml in DMEM culture medium containing 10% FBS and 5 mM BES (SIGMA) were added to a cuvette. After standing for 10 minutes the mixtures were treated with pulse at 0.17kV, 950 $\mu$ F of electric capacity. After the restoration for 10 minutes at room temperature, the electroporated cells were transferred into the DMEM culture medium (10%FBS) in 75 cm<sup>3</sup> flask. After culturing for 72 hours, the culture supernatant was collected and centrifuged to remove cell fragments. The culture supernatant was subjected to the filtration using 0.22  $\mu$ m bottle top filter (FALCON) to obtain the culture supernatant (hereinafter "CM").

#### (2) Preparation of culture supernatant using serum-free culture medium

**[0188]** Cells transfected in the same manner as (1) were transferred to the DMEM medium (10% FBS) in 75 cm<sup>3</sup> flask and cultured overnight. After the culture, the supernatant was discarded and the cells were washed with PBS and then added to CHO-S-SFM II medium (GIBCO BRL). After culturing for 72 hours, the culture supernatant was collected, centrifuged to remove cell fragments and filtered using 0.22  $\mu$ m bottle top filter (FALCON) to obtain CM.

### 6.4 Detection of scFvs and sc(Fv)<sub>2</sub> in CM of COS7

**[0189]** The various MABL2-scFVs and sc(Fv)<sub>2</sub> in CM of COS7 prepared in the aforementioned Example 6.3 (2) were detected by Western Blotting method.

**[0190]** Each CM of COS7 was subjected to SDS-PAGE electrophoresis and transferred to REINFORCED NC membrane (Schleicher & Schuell). The membrane was blocked with 5% skim milk (Morinaga Nyu-gyo) and washed with TBS. Then an anti-FLAG antibody (SIGMA) was added thereto. The membrane was incubated at room temperature and washed. A peroxidase labeled mouse IgG antibody (Jackson Immuno Research) was added. After incubating and washing at room temperature, the substrate solution (Kirkegaard Perry Laboratories) was added to develop color (Fig. 39).

## 6.5 Flow cytometry

**[0191]** Flow cytometry was performed using the culture supernatants of COS7 cells prepared in Example 6.3 (1) to measure the binding of the MABL2-scFVs and sc(Fv)<sub>2</sub> to human Integrin Associated Protein (IAP) antigen. The culture supernatants to be tested or a culture supernatant of COS7 cells as a control was added to  $2 \times 10^5$  cells of the mouse leukemia cell line L1210 expressing human IAP. After incubating on ice and washing, 10 µg/mL of the mouse anti-FLAG antibody (SIGMA) was added and then the cells were incubated and washed. Then, the FITC labeled anti-mouse IgG antibody (BECTON DICKINSON) was added thereto and the cells were incubated and washed again. The fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON). The results of the flow cytometry show that the MABL2-scFVs having linkers with different length and the sc(Fv)<sub>2</sub> in the culture supernatants of COS7 have high affinity to human IAP (see Figs. 40a and 40b).

## 6.6 Apoptosis-inducing Effect in vitro

**[0192]** An apoptosis-inducing action of the culture supernatants of COS7 prepared in Example 6.3 (1) was examined by Annexin-V staining (Boehringer Mannheim) using the L1210 cells transfected with human IAP gene (hIAP/L1210).

**[0193]** To  $5 \times 10^4$  cells of the hIAP/L1210 cells were added the culture supernatants of COS7 cells transfected with each vectors or a culture supernatant of COS7 cells as a control at 10% of the final concentration and the mixtures were cultured for 24 hours. Then, the Annexin-V/PI staining was performed and the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON). The results revealed that scFVs <HL3, 4, 6, 7, LH3, 4, 6, 7> and sc(Fv)<sub>2</sub> in CM of COS7 induced remarkable cell death of hIAP/L1210 cells. These results are shown in Fig. 41.

## 6.7 Construction of vectors for the expression of scFVs and sc(Fv)<sub>2</sub> in CHO cells

**[0194]** To isolate and purify MABL2-scFVs and sc(Fv)<sub>2</sub> from culture supernatant, the expression vectors for expressing in CHO cells were constructed as below.

**[0195]** The EcoRI-BamHI fragments of pCF2HL-0, 3 ~ 7, and pCF2LH-0, 3 ~ 7 prepared in Example 6.2 were introduced between EcoRI and BamHI sites in an expression vector pCHO1 for CHO cells using the Ligation High. Competent *E. coli* DH5α was transformed with them. The plasmids were isolated from the transformed *E. coli* using QIAGEN Plasmid Midi kit (QIAGEN) to prepare expression plasmids pCHOM2HL-0, 3 ~ 7, and pCHOM2LH-0, 3 ~ 7.

## 6.8 Production of CHO cells expressing MABL2-scFVs <HL-0, 3 ~ 7>, MABL2-scFVs <LH-0, 3 ~ 7> and sc(Fv)<sub>2</sub> and preparation of the culture supernatants thereof

**[0196]** CHO cells were transformed with each of the expression plasmids pCHOM2HL-0, 3 ~ 7, and pCHOM2LH-0, 3 ~ 7, constructed in Example 6.7 and pCHOM2(Fv)<sub>2</sub> vector to prepare the CHO cells constantly expressing each modified antibody. As a typical example thereof, the production of the CHO cells constantly expressing MABL2-scFv <HL-5> or sc(Fv)<sub>2</sub> is illustrated as follows.

**[0197]** The expression plasmids pCHOM2HL-5 and pCHON2(Fv)<sub>2</sub> were linearized by digesting with a restriction enzyme PvuI and subjected to transfection to CHO cells by electroporation using Gene Pulser apparatus (BioRad). The DNA (10 µg) and 0.75 ml of PBS with  $1 \times 10^7$  cells/ml were added to a cuvette and treated with pulse at 1.5 kV, 25 µF of electric capacity. After the restoration for 10 minutes at room temperature, the electroporated cells were transferred into nucleic acid-containing α-MEM culture medium (GIBCO BRL) containing 10% fetal bovine serum and cultured. After culturing overnight, the supernatant was discarded. The cells were washed with PBS and added to nucleic acid-free α-MEM culture medium (GIBCO BRL) containing 10% fetal bovine serum. After culturing for two weeks, the cells were cultured in a medium containing 10 nM (final concentration) methotrexate (SIGMA), then 50 nM and 100 nM methotrexate. The resultant cells were cultured in serum-free CHO-S-SFM II medium (GIBCO BRL) in a roller bottle. The culture supernatant was collected, centrifuged to remove cell fragments and filtered using a filter with 0.22 µm of pore size to obtain CM, respectively.

**[0198]** According to the above, CHO cells which constantly express MABL2-scFVs <HL-0, -3, -4, -6, -7> and <LH-0, -3, -4, -5, -6, -7> and CMs thereof were obtained.

## 6.9 Purification of dimer of MABL2-scFv <HL-5> and sc(Fv)<sub>2</sub>

**[0199]** The MABL2-scFv <HL-5> and the sc(Fv)<sub>2</sub> were purified from CMs prepared in Example 6.8 by two types of purification method as below.

## &lt;Purification Method 1&gt;

**[0200]** HL-5 and sc(Fv)<sub>2</sub> were purified by the anti-FLAG antibody affinity column chromatography utilizing the FLAG sequence located at C-terminal of the polypeptides and by gel filtration. One liter of CM as obtained in 6.8 was applied onto a column (7.9ml) prepared with anti-FLAG M2 Affinity gel (SIGMA) equilibrated with 50 mM Tris-HCl buffer (TBS, pH 7.5) containing 150 mM NaCl. After washing the column with TBS, the scFv was eluted by 0.1 M glycine-HCl buffer, pH 3.5. The resultant fractions were analyzed by SDS-PAGE and the elution of the scFv was confirmed. The scFv fraction was mixed with Tween 20 up to 0.01% of the final concentration and concentrated using Centricon-10 (MILLIPORE). The concentrate was applied onto TSKgel G3000SWG column (7.5 × 600 mm) equilibrated with 20 mM acetate buffer (pH 6.0) containing 150 mM NaCl and 0.01% Tween 20. At 0.4 mL/minute of the flow rate, the scFv was detected by the absorption at 280 nm. The HL-5 was eluted as the major fraction in the position of the dimer and the sc(Fv)<sub>2</sub> was eluted in the position of the monomer.

## &lt;Purification Method 2&gt;

**[0201]** HL-5 and sc(Fv)<sub>2</sub> were purified using three steps comprising ion exchange chromatography, hydroxyapatite and gel filtration. In the ion exchange chromatography, Q sepharose fast flow column (Pharmacia) was employed for HL-5 and SP-sepharose fast flow column was employed for sc(Fv)<sub>2</sub>. In and after the second step, HL-5 and sc(Fv)<sub>2</sub> were processed by the same procedure.

First step for HL-5

**[0202]** CM of HL-5 was diluted to two times with 20 mM Tris-HCl buffer (pH 9.0) containing 0.02% Tween 20 and then the pH was adjusted to 9.0 with 1 M Tris. The solution was applied onto Q Sepharose fast flow column equilibrated with 20 mM Tris-HCl buffer (pH 8.5) containing 0.02% Tween 20. A polypeptide adsorbed to the column was eluted by a linear gradient of NaCl in the same buffer, from 0.1 to 0.55 M. Monitoring the eluted fractions by SDS-PAGE, the fractions containing HL-5 were collected and subjected to hydroxyapatite of the second step.

First step for sc(Fv)<sub>2</sub>

**[0203]** CM of the sc(Fv)<sub>2</sub> was diluted to two times with 20mM acetate buffer (pH 5.5) containing 0.02% Tween 20 and its pH was adjusted to 5.5 with 1 M acetic acid. The solution was applied onto a SP-Sepharose fast flow column equilibrated with 20 mM acetate buffer (pH 5.5) containing 0.02% Tween 20. A polypeptide adsorbed to the column was eluted by a linear gradient of NaCl in the buffer, from 0 to 0.5 M. Monitoring the eluted fractions by SDS-PAGE, the fractions containing the sc(Fv)<sub>2</sub> were collected and subjected to hydroxyapatite of the second step.

Second step: Hydroxyapatite chromatography of HL-5 and sc(Fv)<sub>2</sub>

**[0204]** The fractions of HL-5 and sc(Fv)<sub>2</sub> obtained in the first step were separately applied onto the hydroxyapatite column (Type I, BIORAD) equilibrated with 10 mM phosphate buffer containing 0.02% Tween 20, pH 7.0. After washing the column with the same buffer, polypeptides adsorbed to the column were eluted by a linear gradient of the phosphate buffer up to 0.5 M. Monitoring the eluted fractions by SDS-PAGE, the fractions containing the desired polypeptides were collected.

Third step: Gel filtration of HL-5 and sc(Fv)<sub>2</sub>

**[0205]** Each fraction obtained at the second step was separately concentrated with CentriPrep-10 (MILLIPORE) and applied onto a Superdex 200 column (2.6 × 60 cm, Pharmacia) equilibrated with 20 mM acetate buffer (pH 6.0) containing 0.02% Tween 20 and 0.15 M NaCl. HL-5 was eluted in the position of the dimer, and sc(Fv)HL-5 and sc(Fv)<sub>2</sub> were eluted in the position of the monomer as a major peak respectively.

**[0206]** Since the monomer of HL-5 was hardly detected by both purification methods, it is proved that the dimers of single chain Fvs are formed in high yields when the linker for the single chain Fv contains around 5 amino acids. Furthermore, the dimer of HL-5 and the sc(Fv)<sub>2</sub> were stably preserved for a month at 4°C after the purification.

6.10 Evaluation of the binding activity of purified dimer of scFv <HL-5> and sc(Fv)<sub>2</sub> against antigen

**[0207]** Flow cytometry was performed using the purified dimer of MABL2-scFv <HL-5> and the purified sc(Fv)<sub>2</sub> in order to evaluate the binding to human Integrin Associated Protein (IAP). antigen. 10µg/ml of the purified dimer of

MABL2-scFv <HL-5>, the purified sc(Fv)<sub>2</sub>, the antibody MABL-2 as a positive control or a mouse IgG (Zymed) as a negative control was added to  $2 \times 10^5$  cells of the mouse leukemia cell line L1210 expressing human IAP (hIAP/L1210) or the cell line L1210 transformed with pCOS1 (pCOSI/L1210) as a control. After incubating on ice and washing, 10 µg/mL of the mouse anti-FLAG antibody (SIGMA) was added and then the cells were incubated and washed. FITC labeled anti-mouse IgG antibody (BECTON DICKINSON) was added thereto and the cells were incubated and washed again. Then the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON).

**[0208]** Since the purified dimer of MABL2-scFv <HL-5> and the purified sc(Fv)<sub>2</sub> were specifically bound to hIAP/L1210 cells, it is confirmed that the dimer of scFv <HL-5> and the sc(Fv)<sub>2</sub> have high affinity to human IAP (see Fig. 42).

#### 6.11 Apoptosis-inducing activity in vitro of purified dimer of scFv <HL-5> and sc(Fv)<sub>2</sub>

**[0209]** An apoptosis-inducing action of the purified dimer of MABL2-scFv <HL-5> and the purified sc(Fv)<sub>2</sub> were examined by Annexin-V staining (Boehringer Mannheim) using the L1210 cells (hIAP/L1210) in which human IAP gene had been introduced and cells of human leukemic cell line CCRF-CEM.

**[0210]** Different concentrations of the purified dimer of MABL2-scFv <HL-5>, the purified MABL2-sc(Fv)<sub>2</sub>, the antibody MABL-2 as a positive control or a mouse IgG as a negative control were added to  $5 \times 10^4$  cells of hIAP/L1210 cell line or  $1 \times 10^5$  cells of CCRF-CEM cell line. After culturing for 24 hours, the Annexin-V staining was carried out and the fluorescence intensity thereof was measured using the FACScan apparatus (BECTON DICKINSON). As a result the dimer of MABL2-scFv <HL-5> and the MABL2-sc(Fv)<sub>2</sub> remarkably induced cell death of hIAP/L1210 and CCRF-CEM in concentration-dependent manner (see Fig. 43). As a result it was shown that the dimer of MABL2-scFv <HL-5> and MABL2-sc(Fv)<sub>2</sub>, had improved efficacy of inducing apoptosis compared with original antibody MABL-2.

#### 6.12 Hemagglutination Test of the purified dimer of scFv <HL-5> and the sc(Fv)<sub>2</sub>

**[0211]** Hemagglutination test was carried out using different concentrations of the purified dimer of scFv <HL-5> and the purified sc(Fv)<sub>2</sub> in accordance with Example 5.15.

**[0212]** The hemagglutination was observed with the antibody MABL-2 as a positive control, whereas no hemagglutination was observed with both the single chain antibody MABL2-sc(Fv)<sub>2</sub> and the MABL2-scFv <HL-5>. Further, there was no substantial difference in the hemagglutination between two buffers employed with the antibody MABL-2. These results are shown in Table 3.

## Hemagglutination Test

TABLE 3

Diluent : PBS

 $(\mu\text{g/ml})$ 

|                           | cont | 28.9 | 14.45 | 7.225 | 3.6125 | 1.8063 | 0.9031 | 0.4516 | 0.2258 | 0.1129 | 0.0564 | 0.0282 | 0.0141 | 0.0071 | 0.0035 | 0.0018 |
|---------------------------|------|------|-------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| MABL2-sc(Fv) <sub>2</sub> | -    | -    | -     | -     | -      | -      | -      | -      | -      | -      | -      | -      | -      | -      | -      | -      |
| MABL2-sc(Fv)<br><HL5>     | cont | 28.0 | 14.0  | 7.0   | 3.5    | 1.75   | 0.875  | 0.4375 | 0.2188 | 0.1094 | 0.0547 | 0.0273 | 0.0137 | 0.0068 | 0.0034 | 0.0017 |
|                           | -    | -    | -     | -     | -      | -      | -      | -      | -      | -      | -      | -      | -      | -      | -      | -      |
| MABL2 (Intact)            | cont | 80   | 40    | 20    | 10     | 5      | 2.5    | 1.25   | 0.625  | 0.3125 | 0.1563 | 0.0781 | 0.0391 | 0.0195 | 0.0098 | 0.0049 |
|                           | -    | +    | +     | +     | +      | +      | +      | +      | +      | +      | ±      | -      | -      | -      | -      | -      |
| mlgG                      | -    | -    | -     | -     | -      | -      | -      | -      | -      | -      | -      | -      | -      | -      | -      | -      |
| Diluent : Acetate Buffer  |      |      |       |       |        |        |        |        |        |        |        |        |        |        |        |        |
|                           | cont | 80   | 40    | 20    | 10     | 5      | 2.5    | 1.25   | 0.625  | 0.3125 | 0.1563 | 0.0781 | 0.0391 | 0.0195 | 0.0098 | 0.0049 |
| MABL2 (Intact)            | -    | +    | +     | +     | +      | +      | +      | +      | +      | +      | +      | +      | -      | -      | -      | -      |

### 6.13 Antitumor effect of the purified dimer of scFv <HL-5> and the sc(Fv)<sub>2</sub> for a model mouse of human myeloma

**[0213]** The antitumor effects were tested for the dimer of scFv <HL-5> and the sc(Fv)<sub>2</sub> prepared and purified in Examples 6.8 and 6.9. The test was performed by using the mouse model for human myeloma produced in Example 5.1 and determining the amount of M protein produced by human myeloma cells in the mouse serum using ELISA and examining survival time of the mice. Then, the antitumor effects of the dimer of scFv <HL-5> and the sc(Fv)<sub>2</sub> were evaluated in terms of the change of the amount of M protein in the mouse serum and the survival time of the mice.

**[0214]** In the test, the HL-5 and the sc(Fv)<sub>2</sub> were employed as a solution at 0.01, 0.1 or 1 mg/mL in vehicle consisting of 150 mM NaCl, 0.02% Tween and 20 mM acetate buffer, pH 6.0 and administered to the mice at 0.1, 1 or 10 mg/kg of dosage. Control group of mice were administered only with the vehicle.

**[0215]** The mouse serum was gathered 26 days after the transplantation of the human myeloma cells and the amount of M protein in the serum was measured using ELISA according to Example 5.14. As a result, the amount of M protein in the serum of both mice groups administered with HL-5, the dimer and the sc(Fv)<sub>2</sub> decreased in dose-dependent manner (see Fig. 44). Furthermore, a significant elongation of the survival time was observed in both groups administered with the HL-5 (Fig. 45) and with the sc(Fv)<sub>2</sub> (Fig. 46) in comparison with the control group administered with the vehicle. These results show that the HL-5 and the sc(Fv)<sub>2</sub> of the invention have excellent antitumor effect in vivo.

#### Example 7

Single chain Fv comprising H chain V region and L chain V region of human antibody 12B5 against human MPL

**[0216]** A DNA encoding V regions of human monoclonal antibody 12B5 against human MPL was constructed as follows:

#### 7.1 Construction of a gene encoding H chain V region of 12B5

**[0217]** The gene encoding H chain V region of human antibody 12B5 binding to human MPL was designed by connecting the nucleotide sequence of the gene thereof (SEQ ID NO: 55) at the 5'-end to the leader sequence (SEQ ID NO: 56) originated from human antibody gene (Eur. J. Immunol. 1996; 26: 63-69). The designed nucleotide sequence was divided into four oligonucleotides having overlapping sequences of 15 bp each (12B5VH-1, 12B5VH-2, 12B5VH-3, 12B5VH-4). 12B5VH-1 (SEQ ID NO: 57) and 12B5VH-3 (SEQ ID NO: 59) were synthesized in the sense direction, and 12B5VH-2 (SEQ ID NO: 58) and 12B5VH-4 (SEQ ID NO: 60) in the antisense direction, respectively. After assembling each synthesized oligonucleotide by respective complementarity, the outside primers (12B5VH-S and 12B5VH-A) were added to amplify the full length of the gene. 12B5VH-S (SEQ ID NO: 61) was designed to hybridize to 5'-end of the leader sequence by the forward primer and to have Hind III restriction enzyme recognition site and Kozak sequence, and 12B5VH-A (SEQ ID NO: 62) was designed to hybridize to the nucleotide sequence encoding C-terminal of H chain V region by the reverse primer and to have a splice donor sequence and BamHI restriction enzyme recognition site, respectively.

**[0218]** 100μl of the PCR solution containing 10μl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs (dATP, dGTP, dCTP, dTTP), 5 units of DNA-polymerase AmpliTaq Gold (all by PERKIN ELMER) and each 2.5 p mole of each synthesized oligonucleotide (12B5VH-1 to -4) was heated at 94°C of the initial temperature for 9 minutes, at 94°C for 2 minutes, at 55°C for 2 minutes and 72°C for 2 minutes. After repeating the cycle two times each 100 pmole of external primer 12B5VH-S and 12B5VH-A was added. The mixture was subjected to the cycle consisting of at 94°C for 30 seconds, at 55°C for 30 seconds and 72°C for 1 minute 35 times and, heated at 72°C for further 5 minutes.

**[0219]** The PCR product was purified by 1.5% low-melting-temperature agarose gel (Sigma), digested by restriction enzymes BamHI and Hind III, and cloned into expression vector HEF-gγ1 for human H chain. After determining the DNA sequence the plasmid containing the correct DNA sequence was named HEF-12B5H-gγ1.

**[0220]** The HEF-12B5H-gγ1 was digested by restriction enzymes EcoRI and BamHI to produce the gene encoding 12B5VH which was then cloned into an expression vector pCOS-Fd for human Fab H chain to produce pFd-12B5H. The expression vector for human Fab H chain was constructed by amplifying the DNA (SEQ ID NO: 63) containing the intron region existing between the genes encoding human antibody H chain V region and the constant region, and the gene encoding a part of the constant region of human H chain by PCR, and inserting the PCR product into animal cell expression vector pCOS1. The human H chain constant region was amplified for the gene under the same conditions mentioned above using as the template HEF-gγ1, as the forward primer G1CH1-S (SEQ ID NO: 64) which was designed to hybridize to 5'-end sequence of intron 1 and to have restriction enzyme recognition sites EcoRI and BamHI and as the reverse primer G1CH1-A (SEQ ID NO: 65) which was designed to hybridize to 3'-end DNA of human H chain constant region CH1 domain and to have a sequence encoding a part of hinge region, two stop codons and restriction enzyme recognition site Bgl II.

[0221] The nucleotide sequence and amino acid sequence of the reconstructed 12B5H chain variable region which were included in plasmids HEF-12B5H-gy1 and pFd-12B5H are shown in SEQ ID NO: 66.

## 7.2 Construction of the gene encoding 12B5 L chain V region

[0222] The gene encoding L chain V region of human antibody 12B5 binding to human MPL was designed by connecting the nucleotide sequence of gene (SEQ ID NO: 67) at the 5'-end to the leader sequence (SEQ ID NO: 68) originated from human antibody gene 3D6 (Nuc. Acid Res. 1990: 18; 4927). In the same way as mentioned above the designed nucleotide sequence was divided into four oligonucleotides having overlapping sequences of 15 bp each (12B5VL-1, 12B5VL-2, 12B5VL-3, 12B5VL-4) and synthesized respectively. 12B5VL-1 (SEQ ID NO: 69) and 12B5VL-3 (SEQ ID NO: 71) had sense sequences, and 12B5VL-2 (SEQ ID NO: 70) and 12B5VL-4 (SEQ ID NO: 72) had antisense sequences, respectively. Each of the synthesized oligonucleotides was assembled by respective complementarity and mixed with the external primer (12B5VL-S and 12B5VL-A) to amplify the full length of the gene. 12B5VL-S (SEQ ID NO: 73) was designed to hybridize to 5'-end of the leader sequence by the forward primer and to have Hind III restriction enzyme recognition site and Kozak sequence. 12B5VL-A (SEQ ID NO: 74) was designed to hybridize to the nucleotide sequence encoding C-terminal of L chain V region by the reverse primer and to have a splice donor sequence and BamHI restriction enzyme recognition site.

[0223] Performing the PCR as mentioned above, the PCR product was purified by 1.5% low-melting-temperature agarose gel (Sigma), digested by restriction enzymes BamHI and Hind III, and cloned into an expression vector HEF-gk for human L chain. After determining the DNA sequence the plasmid containing the correct DNA sequence was named HEF-12B5L-gk. The nucleotide sequence and amino acid sequence of the reconstructed 12B5 L chain V region which were included in plasmid HEF-12B5L-gk are shown in SEQ ID NO:75.

## 7.3 Production of reconstructed 12B5 single chain Fv (scFv)

[0224] The reconstructed 12B5 antibody single chain Fv was designed to be in the order of 12B5VH-linker-12B5VL and to have FLAG sequence (SEQ ID NO: 76) at C-terminal to facilitate the detection and purification. The reconstructed 12B5 single chain Fv (sc12B5) was constructed using a linker sequence consisting of 15 amino acids represented by (Gly<sub>4</sub>Ser)<sub>3</sub>.

### (1) Production of the reconstructed 12B5 single chain Fv using the linker sequence consisting of 15 amino acids

[0225] The gene encoding the reconstructed 12B5 antibody single chain Fv, which contained the linker sequence consisting of 15 amino acids, was constructed by connecting 12B5 H chain V region, linker region and 12B5 L chain V region which was amplified by PCR respectively. This method is schematically shown in Fig. 47. Six PCR primers (A-F) were used for production of the reconstructed 12B5 single chain Fv. Primers A, C, and E had sense sequences, and primers B, D, and F had antisense sequences.

[0226] The forward primer 12B5-S (Primer A, SEQ ID NO: 77) for H chain V region was designed to hybridize to 5'-end of H chain leader sequence and to have EcoRI restriction enzyme recognition site. The reverse primer HuVHJ3 (Primer B, SEQ ID NO: 78) for H chain V region was designed to hybridize to DNA encoding C-terminal of H chain V region.

[0227] The forward primer RHuJH3 (Primer C, SEQ ID NO: 79) for the linker was designed to hybridize to DNA encoding the N-terminal of the linker and to overlap DNA encoding the C-terminal of H chain V region. The reverse primer RHuVK1 (Primer D, SEQ ID NO: 80) for the linker was designed to hybridize to DNA encoding the C-terminal of the linker and overlap DNA encoding the N-terminal of L chain V region.

[0228] The forward primer HuVK1.2 (Primer E, SEQ ID NO: 81) for L chain V region was designed to hybridize to DNA encoding the N-terminal of L chain V region. The reverse primer 12B5F-A for L chain V region (Primer F, SEQ ID NO: 82) was designed to hybridize to DNA encoding C-terminal of L chain V region and to have the sequence encoding FLAG peptide (Hopp, T. P. et al., Bio/Technology, 6, 1204-1210, 1988), two transcription stop codons and NotI restriction enzyme recognition site.

[0229] In the first PCR step, three reactions A-B, C-D, and E-F were performed, and the three PCR products obtained from the first step PCR were assembled by respective complementarity. After adding primers A and F the full length DNA encoding the reconstructed 12B5 single chain Fv having the linker consisting of 15 amino acids was amplified (the second PCR). In the first step PCR, the plasmid HEF-12B5H-gy1 (see Example 7. 1) encoding the reconstructed 12B5 H chain V region, pSCFVT7-hM21 (humanized ONS-M21 antibody) (Ohtomo et al., Anticancer Res. 18 (1998), 4311-4316) containing DNA (SEQ ID NO: 83) encoding the linker region consisting of Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser (Huston et al., Proc. Natl. Acad. Sci. USA, 85, 5879-5883, 1988) and the plasmid HEF-12B5L-gk (see Example 7. 2) encoding the reconstructed 12B5 L chain V region were used as templates, respectively.

**[0230]** 50µl of PCR solution for the first step contained 5µl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs, 5 units of DNA polymerase AmpliTaq Gold (all by PERKIN ELMER), each 100 pmole of each primer and 100ng of each template DNA. The PCR solution was heated at 94°C of the initial temperature for 9 minutes, at 94 for 30 seconds, 55°C for 30 seconds and 72°C for 1 minute. After repeating the cycle 35 times the reaction mixture was further heated

72°C for 5 minutes.

**[0231]** The PCR products A-B, C-D, and E-F were assembled by the second PCR. PCR mixture solution for the second step of 98µl containing as the template 1µl of the first PCR product A-B, 0.5µl of PCR product C-D and 1µl of PCR product E-F, 10µl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs, 5 units of DNA polymerase AmpliTaq Gold (all by PERKIN ELMER) was heated at 94°C of the initial temperature for 9 minutes, at 94°C for 2 minutes, at 65°C for 2 minutes and 72°C for 2 minutes. After repeating the cycle two times, each 100 pmole of each of primers A and F were added. After repeating the cycle consisting of at 94°C for 30 seconds, 55°C for 30 seconds and 72°C for 1 minute 35 times, the reaction mixture was heated at 72°C for 5 minutes.

**[0232]** The DNA fragments produced by the second PCR were purified using 1.5% low-melting-temperature agarose gel, digested by EcoRI and NotI, and cloned into pCHO1 vector and pCOS1 vector (Japanese Patent Application No. 8-255196). The expression vector pCHO1 was a vector constructed by deleting the antibody gene from DHFR-ΔE-rvH-PM1-f (see WO92/19759) by EcoRI and SmaI digestion, and connecting to EcoRI-NotI-BamHI Adaptor (TAKARA SHUZO). After determining the DNA sequence the plasmids containing the DNA fragment encoding the correct amino acid sequence of reconstructed 12B5 single chain Fv were named pCHO-sc12B5 and pCOS-sc12B5. The nucleotide sequence and amino acid sequence of the reconstructed 12B5 single chain Fv included in the plasmids pCHO-sc12B5 and pCOS-sc12B5 are shown in SEQ ID NO: 84.

#### 7.4 Expression of antibody 12B5 (IgG, Fab) and single chain Fv polypeptide by animal cell

**[0233]** Antibody 12B5 (IgG, Fab) and single chain Fv derived from antibody 12B5 were expressed by using COS-7 cells or CHO cells.

**[0234]** The transient expression using COS-7 cells was performed as follows. The transfection was performed by electroporation method using Gene Pulser equipment (BioRad). For the expression of antibody 12B5 (IgG) each 10µg of the above-mentioned expression vector HEF-12B5H-gy1 and HEF-12 B5L-gk were added, for the expression of 12B5Fab fragment each 10µg of pFd-12B5H and HEF-12B5L-gk were added and for the expression of single chain Fv 10µg of pCOS-sc12B5 was added to COS-7 cells (1x10<sup>7</sup> cells/ml) suspended in 0.8ml of PBS. The mixture kept in a cuvette was treated by pulse at the capacity of 1.5kV, 25µFD. After recovering for 10 minutes in a room temperature the electroporated cells were added to DMEM culture medium (GIBCO BRL) containing 10% bovine fetal serum cultivated. After cultivating overnight the cells were washed once by PBS, added to serum-free medium CHO-S-SFM II and cultivated for 2 days. The culture medium was centrifuged to remove cell debris and filtered with 0.22µm filter to prepare the culture supernatant.

**[0235]** To establish a stable expression CHO cell line for the single chain Fv (polypeptide) derived from antibody 12B5, the expression vector pCHO-sc12B5 was introduced into CHO cells as follows.

**[0236]** The expression vector was introduced into CHO cells by electroporation method using Gene Pulser equipment (BioRad). Linearized DNA (100µg) obtained by digestion with restriction enzyme PvuI and CHO cells (1x10<sup>7</sup> cells/ml) suspended in 0.8 ml of PBS were mixed in a cuvette, left stationary on ice for 10 minutes and treated with pulse at the capacity of 1.5kV, 25µFD. After recovering for 10 minutes at a room temperature the electroporated cells were added to CHO-S-SFM II (GIBCO BRL) containing 10% bovine fetal serum and cultivated. After cultivating for 2 days the cultivation was continued in CHO-S-SFM II (GIBCO BRL) containing 5nM methotrexate (SIGMA) and 10% bovine fetal serum. From thus obtained clones a clone with high expression rate was selected as the production cell line for 12B5 single chain Fv. After cultivating in serum-free medium CHO-S-SFM II (GIBCO BRL) containing 5nM methotrexate (SIGMA), the culture supernatant was obtained by centrifugal separation of cell debris.

#### 7.5 Purification of single chain Fv derived from 12B5 produced by CHO cells

**[0237]** The culture supernatant of CHO cell line expressing 12B5 single chain Fv obtained in 7.4 was purified by anti-FLAG antibody column and gel filtration column.

##### (1) Anti-FLAG antibody column

**[0238]** The culture supernatant was added to anti-FLAG M2 affinity gel (SIGMA) equilibrated by PBS. After washing the column by the same buffer the proteins adsorbed to the column were eluted by 0.1M glycine-HCl buffer (pH 3.5). The eluted fractions were immediately neutralized by adding 1M Tris-HCl buffer (pH 8.0). The eluted fractions were analyzed by SDS-PAGE and the fraction which was confirmed to contain the single chain Fv was concentrated using

Centricon-10 (MILLIPORE).

## (2) Gel filtration

**[0239]** The concentrated solution obtained in (1) was added to Superdex200 column (10x300mm, AMERSHAM PHARMACIA) equilibrated by PBS containing 0.01% Tween20.

The product sc12B5 was eluted in two peaks (A, B) (see Fig. 48). The fractions A and B were analyzed using the 14%-SDS-polyacrylamide gel. The sample was processed by electrophoresis in the presence and absence of a reducing agent according to Laemmli method, and stained by Coomassie Brilliant Blue after the electrophoresis. As shown in Fig. 49 the fractions A and B, regardless of the presence of the reducing agent or its absence, produced a single band having an apparent molecular weight of about 31 kD. When the fractions A and B were analyzed by gel filtration using Superdex200 PC 3.2/30 (3.2x300mm, AMERSHAM PHARMACIA), the fraction A produced an eluted product at an apparent molecular weight of about 44 kD and the fraction B produced at 22kD (see Fig. 50a and b). The results show that the fraction A is the non-covalent bond dimer of sc12B5 single chain Fv, and B is the monomer.

## 7.6 Measurement of TPO-like agonist activity of various single chain Fvs

**[0240]** The TPO-like activity of anti-MPL single chain antibody was evaluated by measuring the proliferation activity to Ba/F3 cells (BaF/mpl) expressing human TPO receptor (MPL). After washing BaF/Mpl cells two times by RPMI1640 culture medium (GIBCO) containing 10% bovine fetal serum (GIBCO), the cells were suspended in the culture medium at cell density of  $5 \times 10^5$  cells/ml. The anti-MPL single chain antibody and human TPO (R&D Systems) was diluted with the culture medium, respectively. 50 $\mu$ l of the cell suspension and 50 $\mu$ l of the diluted antibody or human TPO were added in 96-well microplate (flat bottom) (Falcon), and cultivated in CO<sub>2</sub> incubator (CO<sub>2</sub> concentration: 5%) for 24 hours. After the incubation 10 $\mu$ l of WST-8 reagent (reagent for measuring the number of raw cells SF: Nacalai Tesque) was added and the absorbance was immediately measured at measurement wavelength of 450nm and at reference wavelength of 620nm using fluorescence absorbency photometer SPECTRA Fluor (TECAN). After incubating in CO<sub>2</sub> incubator (CO<sub>2</sub> concentration: 5%) for 2 hours, the absorbance at 450nm of measurement wavelength and 620nm of reference wavelength was again measured using SPECTRA Fluor. Since WST-8 reagent developed the color reaction depending upon the number of live cells at wavelength of 450nm, the proliferation activity of BaF/Mpl based on the change of absorbance in 2 hours was evaluated by ED 50 calculated as follows. In the proliferation reaction curve wherein the absorbance was plotted on the ordinate against the antibody concentration on the abscissa, the absorbance at the plateau was set 100% reaction rate. Obtaining an approximation formula by straight line approximation method based on the plotted values close to 50% reaction rate, the antibody concentration of 50% reaction rate was calculated and adopted as ED 50.

The results of the agonist activity to MPL measured by using culture supernatants of COS-7 cells expressing various 12B5 antibody molecules showed as illustrated in Fig. 51 that 12B5IgG having bivalent antigen-binding site increased the absorbance in concentration-dependent manner and had TPO-like agonist activity (ED50; 29nM), while the agonist activity of 12B5Fab having monovalent antigen-binding site was very weak (ED50; 34,724nM). On the contrary the single chain Fv (sc12B5) having monovalent antigen-binding site like Fab showed strong agonist activity at a level that ED50 was 75nM. However it has been known that variable regions of H chain and L chain of the single chain Fv are associated through non-covalent bond and, therefore, each variable region is dissociated in a solution and can be associated with variable region of other molecule to form multimers like dimers. When the molecular weight of sc12B5 purified by gel filtration was measured, it was confirmed that there were molecules recognized to be monomer and dimer (see Fig. 48). Then monomer sc12B5 and dimer sc12B5 were isolated (see Fig. 50) and measured for the agonist activity to MPL. As shown in Figs. 51 and 52, ED50 of sc12B5 monomer was 4438.7nM, which confirmed that the agonist activity was reduced compared with the result using culture supernatant of COS-7 cells. On the contrary single chain Fv (sc12B5 dimer) having bivalent antigen-binding site showed about 400-fold stronger agonist activity (ED50; 10.1nM) compared with monovalent sc12B5. Furthermore, the bivalent single chain Fv showed the agonist activity equivalent to or higher than the agonist activity of human TPO and 12B5IgG.

## Example 8

Construction of a gene encoding the variable region of human antibody 12E10 against human MPL

**[0241]** A DNA encoding variable region of human monoclonal antibody 12E10 against human MPL was constructed as follows:

## 8.1 Construction of a gene encoding 12E10 H chain V region

**[0242]** The nucleotide sequence SEQ ID NO:86 was designed as a gene encoding H chain V region of human antibody 12E10 binding to human MPL on the basis of the amino acid sequence described in WO99/1049 (SEQ ID NO: 85). The full length of nucleotide sequence was designed by connecting to its 5'-end the leader sequence (SEQ ID NO:87) derived from human antibody gene (GenBank accession No. AF062252). The designed nucleotide sequence was divided into four oligonucleotides having overlapping sequences of 15 bp each (12E10VH1, 12E10VH2, 12E10VH3, 12E10VH4). 12E10VH1 (SEQ ID NO: 88) and 12E10VH3 (SEQ ID NO: 90) were synthesized in the sense direction, and 12E10VH2 (SEQ ID NO: 89) and 12E10VH4 (SEQ ID NO: 91) in the antisense direction, respectively. After assembling each synthesized oligonucleotide by respective complementarity, the external primers (12E10VHS and 12E10VHA) were added to amplify the full length of the gene. 12E10VHS (SEQ ID NO: 92) was designed to hybridize to 5'-end of the leader sequence by the forward primer and to have Hind III restriction enzyme recognition site and Kozak sequence, and 12E10VHA (SEQ ID NO: 93) was designed to hybridize to the nucleotide sequence encoding C-terminal of H chain V region by the reverse primer and to have a splice donor sequence and BamHI restriction enzyme recognition site, respectively.

**[0243]** 100 µl of the PCR solution containing 10µl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs (dATP, dGTP, dCTP, dTTP), 5 units of DNA-polymerase AmpliTaq Gold (all by PERKIN ELMER) and each 2.5pmole of each synthesized oligonucleotide (12B5VH-1 to -4) was heated at 94°C of the initial temperature for 9 minutes, at 94°C for 2 minutes, at 55°C for 2 minutes and 72°C for 2 minutes. After repeating the cycle two times each 100 pmole of external primer 12E10VHS and 12E10VHA were added. The mixture was subjected to the cycle consisting of at 94°C for 30 seconds, at 55°C for 30 seconds and 72°C for 1 minute 35 times and heated at 72°C for further 5 minutes.

**[0244]** The PCR product was purified by 1.5% low-melting-temperature agarose gel (Sigma), digested by restriction enzymes BamHI and Hind III, and cloned into a human H chain expression vector HEF-gγ1. After determining the DNA sequence the plasmid containing the correct DNA sequence was named HEF-12E10H-gγ1.

**[0245]** The HEF-12E10H-gγ1 was digested by restriction enzymes EcoRI and BamHI to produce the gene encoding 12E10VH and then cloned into a human Fab H chain expression vector pCOS-Fd to produce pFd-12E10H. The human Fab H chain expression vector was constructed by amplifying the DNA (SEQ ID NO: 63) containing the intron region existing between the genes encoding human antibody H chain V region and the constant region, and the gene encoding a part of the human H chain constant region by PCR, and inserting the PCR product into animal cell expression vector pCOS1. The human H chain constant region was amplified for the gene under the same conditions mentioned above using as the template HEF-gγ1, as the forward primer G1CH1-S (SEQ ID NO: 64) which was designed to hybridize to 5'-end sequence of intron 1 and to have restriction enzyme recognition sites EcoRI and BamHI and as the reverse primer G1CH1-A (SEQ ID NO: 65) which was designed to hybridize to 3'-end DNA of human H chain constant region CH1 domain and to have a sequence encoding a part of hinge region, two stop codons and restriction enzyme recognition site Bg1 II.

**[0246]** The nucleotide sequence and amino acid sequence of the reconstructed 12E10 H chain variable region which were included in plasmids HEF-12E10H-gγ1 and pFd-12E10H are shown in SEQ ID NO: 94.

## 8.2 Construction of a gene encoding 12E10 L chain V region

**[0247]** The nucleotide sequence SEQ ID NO:96 was designed as a gene encoding L chain V region of human antibody 12E10 binding to human MPL on the basis of the amino acid sequence described in WO99/1049 (SEQ ID NO:95). It was further designed by connecting to its 5'-end the leader sequence (SEQ ID NO: 97) derived from human antibody gene (Mol. Immunol. 1992; 29: 1515-1518). In the same way as mentioned above the designed nucleotide sequence was divided into four oligonucleotides having overlapping sequences of 15 bp each (12E10VL1, 12E10VL2, 12E10VL3, 12E10VL4) and synthesized respectively. 12E10VL1 (SEQ ID NO: 98) and 12E10VL3 (SEQ ID NO: 100) had sense sequences, and 12E10VL2 (SEQ ID NO: 99) and 12E10VL4 (SEQ ID NO: 101) had antisense sequences, respectively. Each of the synthesized oligonucleotides was assembled by respective complementarity and mixed with the external primers (12E10VLS and 12E10VLA) to amplify the full length of the gene. 12E10VLS (SEQ ID NO: 102) was designed to hybridize to 5'-end of the leader sequence by the forward primer and to have EcoRI restriction enzyme recognition site and Kozak sequence. 12E10VLA (SEQ ID NO: 103) was designed to hybridize to the nucleotide sequence encoding C-terminal of L chain V region by the reverse primer and to have a BlnI restriction enzyme recognition site.

**[0248]** Performing the PCR as mentioned above, the PCR product was purified by 1.5% low-melting-temperature agarose gel (Sigma), digested by restriction enzymes EcoRI and BlnI, and cloned into pUC19 containing a gene for human lambda chain constant region. After determining the DNA sequence the plasmid containing the correct DNA sequence was digested by EcoRI to produce a gene encoding 12E10 L chain V region and human lambda chain constant region and then inserted in expression vector pCOS1. The plasmid having 12E10 L chain gene (SEQ ID NO: 104) was named pCOS-12E10L.

## 8.3 Production of reconstructed 12E10 single chain Fv

**[0249]** The reconstructed 12E10 antibody single chain Fv was designed to be in the order of 12E10VH-linker-12E10VL and to have FLAG sequence (SEQ ID NO: 105) at C-terminal to facilitate the detection and purification. The reconstructed 12E10 chain Fvs (sc12E10 and db12E10) were constructed using a linker sequence consisting of 15 amino acids represented by (Gly<sub>4</sub>Ser)<sub>3</sub> or 5 amino acids represented by (Gly<sub>4</sub>Ser)<sub>1</sub>.

(1) Production of the reconstructed 12E10 single chain Fv using the linker sequence consisting of 5 amino acids

**[0250]** The gene encoding the reconstructed 12E10 single chain Fv, which contained the linker sequence consisting of 5 amino acids, was constructed by introducing the nucleotide sequence for the linker (Gly<sub>4</sub>Ser)<sub>1</sub> to 3'-end of the gene encoding 12E10 H chain V region and to 5'-end of the gene encoding 12E10 L chain V region, amplifying thus obtained respective gene by PCR and connecting the amplified genes. Four PCR primers (A-D) were used to produce the reconstructed 12E10 single chain Fv. Primers A and C had sense sequences, and primers B and D had antisense sequences.

**[0251]** The forward primer for H chain V region was 12E10S (Primer A, SEQ ID NO: 106). The reverse primer DB2 (Primer B, SEQ ID NO: 107) for H chain V region was designed to hybridize to DNA encoding C-terminal of H chain V region and to have the nucleotide sequence encoding the linker (Gly<sub>4</sub>Ser)<sub>1</sub> and the nucleotide sequence encoding N-terminal of L chain V region.

**[0252]** The forward primer DB1 (Primer C, SEQ ID NO: 108) for L chain V region was designed to hybridize to DNA encoding the N-terminal of L chain V region and to have the nucleotide sequence encoding the linker (Gly<sub>4</sub>Ser)<sub>1</sub> and the nucleotide sequence encoding C-terminal of H chain V region. The reverse primer 12E10FA (Primer D, SEQ ID NO: 109) for L chain V region was designed to hybridize to DNA encoding the C-terminal of L chain V region and to have the nucleotide sequence encoding FLAG and NotI restriction enzyme recognition site.

**[0253]** In the first PCR step, two reactions A-B and C-D were performed, and the two PCR products obtained from the first step PCR were assembled by respective complementarity. After adding primers A and D the full length DNA encoding the reconstructed 12E10 single chain Fv having the linker consisting of 5 amino acids was amplified (the second PCR). In the first step PCR, the plasmid HEF-12E10H-gy1 (see Example 8. 1) encoding the reconstructed 12E10 H chain V region and pCOS-12E10L (see Example 8.1) encoding the reconstructed 12E10 L chain V region were used as templates, respectively.

**[0254]** 50μl of the first step PCR solution contained 5μl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs, 5 units of DNA polymerase AmpliTaq Gold (by PERKIN ELMER), each 100 pmole of each primer and 100ng of each template DNA. The PCR solution was heated at 94°C of the initial temperature for 9 minutes, at 94 for 30 seconds, 55°C for 30 seconds and 72°C for 1 minute. After repeating the cycle 35 times the reaction mixture was further heated at 72°C for 5 minutes.

**[0255]** The PCR products A-B (429bp) and C-D (395bp) were assembled by the second PCR. The second step PCR mixture solution (98μl) containing 1μl each of the first PCR product A-B and C-D as templates, 100 pmole each of each primer, 10μl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs and 5 units of DNA polymerase AmpliTaq Gold (by PERKIN ELMER) was reacted under the same conditions as mentioned above.

**[0256]** The DNA fragment of 795bp produced by the second PCR was purified using 1.5% low-melting-temperature agarose gel, digested by EcoRI and NotI, and cloned into pCHO1 vector or pCOS1 vector. The expression vector pCHO1 was a vector constructed by deleting the antibody gene from DHFR-ΔE-RVH-PM1-f (see WO92/19759) by EcoRI and SmaI digestion, and connecting to EcoRI-NotI-BamHI Adaptor (TAKARA SHUZO). After determining the DNA sequence the plasmids containing the DNA fragment encoding the correct amino acid sequence of reconstructed 12B5 single chain Fv were named pCHO-db12E10 and pCOS-db12E10. The nucleotide sequence and amino acid sequence of the reconstructed 12E10 single chain Fv included in the plasmids pCHO-db12E1 and pCOS-db12E10 are shown in SEQ ID NO: 110.

(2) Production of the reconstructed 12E10 single chain Fv using the linker sequence consisting of 15 amino acids

**[0257]** The gene encoding the reconstructed 12E10 antibody single chain Fv, which contained the linker sequence consisting of 15 amino acids, was constructed by introducing the nucleotide sequence for the linker (Gly<sub>4</sub>Ser)<sub>3</sub> to 3'-end of the gene encoding 12E10 H chain V region and to 5'-end of the gene encoding 12E10 L chain V region, amplifying thus obtained respective gene by PCR and connecting the amplified genes. Four PCR primers (A-D) were used for production of the reconstructed 12E10 single chain Fv. Primers A and C had sense sequences, and primers B and D had antisense sequences.

**[0258]** The forward primer for H chain V region was 12E10S (Primer A, SEQ ID NO: 106). The reverse primer sc4.3 (Primer B, SEQ ID NO: 111) for H chain V region was designed to hybridize to DNA encoding C-terminal of H chain V

region and to have the nucleotide sequence encoding the linker (Gly<sub>4</sub>Ser)<sub>3</sub> and the nucleotide sequence encoding N-terminal of L chain V region.

**[0259]** The forward primer sc1.3 (Primer C, SEQ ID NO: 112) for L chain V region was designed to hybridize to DNA encoding the N-terminal of L chain V region and to have the nucleotide sequence encoding the linker (Gly<sub>4</sub>Ser)<sub>3</sub> and the nucleotide sequence encoding C-terminal of H chain V region. The reverse primer 12E10FA (Primer D, SEQ ID NO: 109) for L chain V region was designed to hybridize to DNA encoding the C-terminal of L chain V region and to have the nucleotide sequence encoding FLAG and NotI restriction enzyme recognition site.

**[0260]** In the first PCR step, two reactions A-B and C-D were performed, and the two PCR products obtained from the first step PCR were assembled by respective complementarity. After adding primers A and D the full length DNA encoding the reconstructed 12E10 single chain Fv having the linker consisting of 15 amino acids was amplified (the second PCR). In the first step PCR, the plasmid pCOS-db12E10 (see Example 8. 1(1)) encoding the reconstructed 12E10 single chain Fv was used as template.

**[0261]** 50μl of the first step PCR solution contained 5μl of 10 x ExTaq Buffer, 0.4mM dNTPs, 2.5 units of DNA polymerase TaKaRa ExTaq (by TAKARA), each 100 pmole of each primer and 10ng of each template DNA. The PCR solution was heated at 94°C of the initial temperature for 30 seconds, at 94 for 15 seconds and 72°C for 2 minute, and the cycle was repeated 5 times. After repeating 28 times the cycle of at 94°C for 15 seconds and at 70°C for 2 minutes, the reaction mixture was further heated at 72°C for 5 minutes.

**[0262]** The PCR products A-B (477bp) and C-D (447bp) were assembled by the second PCR. The second step PCR mixture solution (98μl) containing 1μl each of the first PCR products A-B and C-D as templates, 100 pmole each of each primer A and D, 5μl of 10 x ExTaq Buffer, 0.4mM dNTPs, 2.5 units of DNA polymerase TaKaRa ExTaq (by TAKARA) was reacted under the same conditions as mentioned above.

**[0263]** The DNA fragment of 825bp produced by the second PCR was purified using 1.0% low-melting-temperature agarose gel, digested by EcoRI and NotI. Thus obtained DNA fragment was cloned into pCHO1 vector or pCOS1 vector. After determining the DNA sequence the plasmids containing the DNA fragment encoding the correct amino acid sequence of reconstructed 12E10 single chain Fv were named pCHO-sc12E10 and pCOS-sc12E10. The nucleotide sequence and amino acid sequence of the reconstructed 12E10 single chain Fv included in the plasmids pCHO-sc12E10 and pCOS-sc12E10 are shown in SEQ ID NO: 113.

#### 8.4 Expression of antibody 12E10 (IgG, Fab) and single chain Fv polypeptide by animal cell

**[0264]** Antibody 12E10 (IgG, Fab) and single chain Fv derived from antibody 12E10 (linker sequence 5 amino acids, 15 amino acids) were expressed by using COS-7 cells or CHO cells.

**[0265]** The transient expression using COS-7 cells was performed as follows. The transfection was performed by electroporation method using Gene Pulser II equipment (BioRad). For the expression of antibody 12E10 (IgG) each 10μg of the above-mentioned expression vector HEF-12E10H-gγ1 and pCOS-12E10L were added, for the expression of 12E10Fab fragment each 10μg of pFd-12E10H and pCOS-12E10L were added and for the expression of single chain Fv of pCOS-sc12E10 (10μg) or pCOS-db12E10 (10μg) was added to COS-7 cells (1×10<sup>7</sup> cells/ml) suspended in 0.8ml of PBS. The mixture kept in a cuvette was treated by pulse at the capacity of 1.5kV, 25μFD. After recovering for 10 minutes in a room temperature the electroporated cells were added to DMEM medium (GIBCO BRL) containing 10% bovine fetal serum and cultivated. After cultivating overnight the cells were washed once by PBS, added to serum-free medium CHO-S-SFM II (GIBCO BRL) and cultivated for 3 days. The culture supernatant was centrifuged to remove cell debris and filtered with 0.22μm filter.

**[0266]** To establish a stable expression CHO cell line for the single chain Fv (polypeptide) derived from antibody 12E10, the expression vector pCHO-sc12E10 or pCHO-ds12E10 was introduced into CHO cells respectively.

**[0267]** Each expression vector was introduced into CHO cells by electroporation method using Gene Pulser II equipment (BioRad). Linearized DNA (100μg) obtained by digestion with restriction enzyme PvuI and CHO cells (1×10<sup>7</sup> cells /ml) suspended in 0.8 ml of PBS were mixed in a cuvette, left stationary on ice for 10 minutes and treated with pulse at the capacity of 1.5kV, 25μFD. After recovering for 10 minutes at a room temperature the electroporated cells were added to CHO-S-SFM II medium (GIBCO BRL) containing 10% dialyzed bovine fetal serum and nucleic acid and cultivated. After cultivating for 2 days the cultivation was continued in nucleic acid-free CHO-S-SFM II medium (GIBCO BRL) containing 10% dialyzed bovine fetal serum. From thus obtained clones a clone with high expression rate was selected as the production cell line for 12E10 single chain Fv. After cultivating in serum-free CHO-S-SFM II medium (GIBCO BRL), the culture supernatant was centrifuged to remove cell debris and filtered with 0.22μm filter.

#### 8.5 Purification of single chain Fv derived from 12E10 produced by CHO cells

**[0268]** The culture supernatants produced by CHO cell lines expressing 12E10 single chain Fvs (sc12E10 db12E10) obtained in Example 8.4 were purified by anti-FLAG antibody column and gel filtration column respectively to produce

purified single chain Fvs.

#### (1) Purification with anti-FLAG antibody column

**[0269]** Each culture supernatant (sc12E10 db12E10) was added to anti-FLAG M2 affinity gel column (SIGMA) equilibrated by 50mM Tris-HCl buffer (pH7.4) containing 150mM NaCl. After washing the column by the same buffer the proteins adsorbed to the column were eluted by 100mM glycine buffer (pH 3.5). The eluted fractions were immediately neutralized by adding 1M Tris-HCl buffer (pH 8.0) and analyzed by SDS-PAGE. The fraction which was confirmed to contain the single chain Fv was pooled and concentrated about 20-fold using Centricon-10 (AMICON).

#### (2) Gel filtration

**[0270]** The concentrated solution obtained in (1) was added to Superdex200 column HR (10x300mm, AMERSHAM PHARMACIA) equilibrated by PBS containing 0.01% Tween20. Chromatograms were shown in Fig. 53 and 54. The product sc12E10 was eluted in two peaks (A, B) (see Fig. 53). The product db12E10 was eluted in two peaks (C, D) (see Fig. 54). Each peak fraction was collected, treated in the presence and absence of a reducing agent, processed by electrophoresis according to Laemmli method and stained by Coomassie Brilliant Blue after the electrophoresis. As shown in Fig. 55 the all of fractions A, B, C and D, regardless of the presence or absence of the reducing agent, produced a single band having an apparent molecular weight of about 31 kD. When these fractions were analyzed by gel filtration using Superdex200 HR, the fraction A produced a product eluted at an apparent molecular weight of about 20 kD, the fraction B at 42kD (see Fig. 56), fraction C at 69kD and fraction D at 41kD (see Fig. 57). The results suggest that sc12E10-derived fraction A is the non-covalent bond dimer of single chain Fv and the fraction B is the monomer of single chain Fv, and the db12E10-derived fraction C is the non-covalent bond trimer of single chain Fv and D is non-covalent bond dimer of single chain Fv.

#### 8.6 Measurement of TPO-like agonist activity of various single chain Fvs

**[0271]** The TPO-like activity of anti-mpl single chain antibody was evaluated by measuring the proliferation activity to Ba/F3 cells (BaF/mpl) expressing human TPO receptor (MPL).

**[0272]** After washing BaF/mpl cells two times by RPMI1640 medium (GIBCO) containing 1% bovine fetal serum (GIBCO), the cells were suspended in the medium at cell density of  $5 \times 10^5$  cells/mL. The anti-MPL single chain antibody or human TPO (R&D Systems) was diluted with the medium, respectively. 50 $\mu$ l of the cell suspension and 50 $\mu$ l of the diluted antibody or human TPO were added in 96-well microplate (flat bottom) (Corning), and cultivated in CO<sub>2</sub> incubator (CO<sub>2</sub> concentration: 5%) for 24 hours. After the incubation 10 $\mu$ l of WST-8 reagent (reagent for measuring the number of raw cells SF: Nacalai Tesque) was added and the absorbance was immediately measured at measurement wavelength of 450nm and at reference wavelength of 655nm using absorbency photometer Benchmark Plus (BioRad). After incubating in CO<sub>2</sub> incubator (CO<sub>2</sub> concentration: 5%) for 2 hours, the absorbance at 450nm of measurement wavelength and 655nm of reference wavelength was again measured using Benchmark Plus. Since WST-8 reagent developed the color reaction depending upon the number of live cells at wavelength of 450nm, the proliferation activity of BaF/mpl was evaluated based on the change of absorbance in 2 hours.

**[0273]** The agonist activity to MPL measured by using culture supernatants of COS-7 cells expressing various 12E10 antibody molecules are shown in Fig. 58. Single chain Fvs having the 5-amino-acid-linker (ds12E10 and the 15-amino-acid-linker (sc12E10 increased the absorbance in concentration-dependent manner, showing TPO-like agonist activity (ED50; 9pM and 51pM respectively), while 12E10IgG and 12E10Fab had no activity.

**[0274]** It has been known that H chain and L chain of the single chain Fv are associated not only within a molecule but also between molecules to form multimers such as dimer. When the culture supernatants of CHO cells expressing single chain Fvs of 12E10 were gel filtrated and tested for agonist activity on MPL. The results were shown in Fig. 59. The dimer, which was contained in sc12E10 in a small amount, showed about 5000-fold stronger TPO-like agonist activity (sc12E10 dimer, ED50; 1.9pM) compared with the monomer (sc12E10 monomer, ED50; >10nM). The activity was higher than that of TPO (ED50; 27pM). The dimer of db12E10 (db12E10 dimer, ED50; 2.0pM) showed strong activity comparable to that of sc12E10 dimer. db12E10 trimer (ED50; 7.4pM), which was presumed to be a trimer from molecular weight obtained by gel filtration, showed a high activity which is lower than that of db12E10 dimer. Those results suggest that it is important for the activity of agonist antibody 12E10 that the antigen-binding site is bivalent (dimer). Considering the fact that 12E10 IgG had no activity, other factors than being bivalent are presumed to be important such as the location of antigen-binding site, the distance or the angle.

## EXPLANATION OF DRAWINGS

[0275] Fig. 1 shows the result of flow cytometry, illustrating that human IgG antibody does not bind to L1210 cells expressing human IAP (hIAP/L1210).

[0276] Fig. 2 shows the result of flow cytometry, illustrating that the chimera MABL-1 antibody specifically binds to L1210 cells expressing human IAP (hIAP/L1210).

[0277] Fig. 3 shows the result of flow cytometry, illustrating that the chimera MABL-2 antibody specifically binds to L1210 cells expressing human IAP (hIAP/L1210).

[0278] Fig. 4 schematically illustrates the process for producing the single chain Fv according to the present invention.

[0279] Fig. 5 illustrates a structure of an expression plasmid which can be used to express a DNA encoding the single chain Fv of the invention in *E. coli*.

[0280] Fig. 6 illustrates a structure of an expression plasmid which is used to express a DNA encoding the single chain Fv of the invention in mammalian cells.

[0281] Fig. 7 shows the result of western blotting in Example 5.4. From the left, a molecular weight marker (which indicates 97.4, 66, 45, 31, 21.5 and 14.5 kDa from the top), the culture supernatant of pCHO1-introduced COS7 cells and the culture supernatant of pCHOM2-introduced COS7 cells. It illustrates that the reconstructed single chain Fv of the antibody MABL-2 (arrow) is contained in the culture supernatant of the pCHOM2-introduced cells.

[0282] Fig. 8 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of pCHO1/COS7 cell as a control does not bind to pCOS1/L1210 cell as a control.

[0283] Fig. 9 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of MABL2-scFv/COS7 cells does not bind to pCOS1/L1210 cells as a control.

[0284] Fig. 10 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of pCOS1/COS7 cells as a control does not bind to hIAP/L1210 cells.

[0285] Fig. 11 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of MABL2-scFv/COS7 cells specifically binds to hIAP/L1210 cells.

[0286] Fig. 12 shows the result of the competitive ELISA in Example 5.6, wherein the binding activity of the single chain Fv of the invention (MABL2-scFv) to the antigen is demonstrated in terms of the inhibition of binding of the mouse monoclonal antibody MABL-2 to the antigen as an index, in comparison with the culture supernatant of pCHO1/COS7 cells as a control.

[0287] Fig. 13 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of pCHO1/COS7 cells as a control does not induce the apoptosis of pCOS1/L1210 cells as a control.

[0288] Fig. 14 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of MABL2-scFv/COS7 cells does not induce apoptosis of pCOS1/L1210 cells as a control.

[0289] Fig. 15 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of pCHO1/COS7 cells as a control does not induce apoptosis of hIAP/L1210 cells.

[0290] Fig. 16 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of MABL2-scFv/COS7 cells specifically induces apoptosis of hIAP/L1210 cells.

[0291] Fig. 17 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of pCHO1/COS7 cells as a control does not induce apoptosis of CCRF-CEM cells (at 50% of the final concentration).

[0292] Fig. 18 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of MABL2-scFv/COS7 cells specifically induces apoptosis of CCRF-CEM cells (at 50% of the final concentration).

[0293] Fig. 19 shows the chromatogram obtained in the purification of the single chain Fv derived from the antibody MABL-2 produced by the CHO cells in Example 5.9, illustrating that fraction A and fraction B were obtained as the major peaks when the fraction from Blue-sepharose column was purified with hydroxyapatite column.

[0294] Fig. 20 shows the results of purification by gel filtration of fraction A and fraction B obtained in Example 5.9-(2), illustrating that the major peaks (AI and BI, respectively) were eluted from fraction A at approximately 36 kD of the apparent molecular weight and from fraction B at approximately 76 kD.

[0295] Fig. 21 is the analysis on SDS-PAGE of the fractions obtained in the purification of the single chain Fv derived from the antibody MABL-2 produced by the CHO cells in Example 5.9, illustrating that a single band of approximately 35 kD of molecular weight was observed in both fractions.

[0296] Fig. 22 shows the results of analysis of fractions AI and BI obtained by gel filtration in the purification of the single chain Fv derived from the antibody MABL-2 produced by the CHO cells, wherein fraction AI comprises monomer and fraction BI comprises dimer.

[0297] Fig. 23 illustrates a structure of an expression plasmid which can be used to express a DNA encoding the single chain Fv of the invention in *E. coli*.

[0298] Fig. 24 shows the results of purification on the gel filtration column of crude products of the single chain Fv

polypeptide derived from the antibody MABL-2 produced by *E. coli* obtained in Example 5.12, wherein each peak indicates monomer or dimer, respectively, of the single chain Fv produced by *E. coli*.

**[0299]** Fig. 25 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that mouse IgG antibody as a control does not induce apoptosis of hIAP/L1210 cells (the final concentration of 3 µg/ml).

**[0300]** Fig. 26 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that the dimer of MABL2-scFv produced by the CHO cells remarkably induces apoptosis of hIAP/L1210 cells (the final concentration of 3 µg/ml).

**[0301]** Fig. 27 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that the dimer of MABL2-scFv produced by *E. coli* remarkably induces apoptosis of hIAP/L1210 cells (the final concentration of 3 µg/ml).

**[0302]** Fig. 28 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that apoptosis induction to hIAP/L1210 cells by the MABL2-scFv monomer produced by the CHO cells is the same level as that of the control (the final concentration of 3 µg/ml).

**[0303]** Fig. 29 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that apoptosis induction to hIAP/L1210 cells of the MABL2-scFv monomer produced by *E. coli* is the same level as that of control (the final concentration of 3 µg/ml).

**[0304]** Fig. 30 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that mouse IgG antibody used as a control does not induce apoptosis of hIAP/L1210 cells even when anti-FLAG antibody is added (the final concentration of 3 µg/ml).

**[0305]** Fig. 31 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that MABL2-scFv monomer produced by the CHO cells remarkably induces apoptosis of hIAP/L1210 cells when anti-FLAG antibody is added (the final concentration of 3 µg/ml).

**[0306]** Fig. 32 shows the results of quantitative measurement of human IgG in the serum of a human myeloma cell line KPMM2-transplanted mouse, indicating amounts of human IgG produced by the human myeloma cells in the mouse. It illustrates that the dimer of scFv/CHO remarkably inhibited growth of the KPMM2 cells.

**[0307]** Fig. 33 shows the survival time of the mouse after the transplantation of tumor, illustrating that the scFv/CHO dimer-administered group elongated remarkably the survival time.

**[0308]** Fig. 34 illustrates a structure of an expression plasmid which expresses a modified antibody [sc(Fv)<sub>2</sub>] comprising two H chain V regions and two L chain V regions derived from the antibody MABL-2.

**[0309]** Fig. 35 illustrates a structure of a plasmid which expresses a scFv (HL type) wherein the V regions are linked in the manner of [H chain]-[L chain] without a peptide linker.

**[0310]** Fig. 36 illustrates a structure of the HL-type polypeptide and amino acid sequences of peptide linkers.

**[0311]** Fig. 37 illustrates a structure of a plasmid which expresses a scFv (LH type) wherein the V regions are linked in the manner of [L chain]-[H chain] without a peptide linker.

**[0312]** Fig. 38 illustrates a structure of the LH-type polypeptide and amino acid sequences of peptide linkers.

**[0313]** Fig. 39 shows the results of the western blotting in Example 6.4, illustrating that the modified antibody sc(Fv)<sub>2</sub> comprising two H chain V regions and two L chain V regions, and the MABL2-scFv having peptide linkers with different length are expressed.

**[0314]** Figs. 40a and 40b show the results of flow cytometry using the culture supernatant of COS7 cells prepared in Example 6.3 (1), illustrating that the MABL2-scFv and sc(Fv)<sub>2</sub> having peptide linkers with different length have high affinities against human IAP.

**[0315]** Fig. 41 shows the results of the apoptosis-inducing effect in Example 6.6, illustrating that the scFv <HL3, 4, 6, 7, LH3, 4, 6 and 7> and the sc(Fv)<sub>2</sub> remarkably induce cell death of hIAP/L1210 cells.

**[0316]** Fig. 42 shows the results of the evaluation of antigen binding capacity in Example 6.10, illustrating that the dimer of scFv <HL5> and sc(Fv)<sub>2</sub> have high affinities against human IAP.

**[0317]** Fig. 43 shows the results of the *in vitro* apoptosis-inducing effect in Example 6.11, illustrating that the dimer of scFv <HL5> and the sc(Fv)<sub>2</sub> induce apoptosis of hIAP/L1210 cells and CCRF-CEM cells in concentration-dependent manner.

**[0318]** Fig. 44 shows the results of the quantitative measurement of M protein produced by a human myeloma cell line KPMM2 in the serum of the human myeloma cell-transplanted mouse. It illustrates that the dimer of scFv <HL5> and the sc(Fv)<sub>2</sub> remarkably inhibited growth of the KPMM2 cells.

**[0319]** Fig. 45 shows the survival time (days) of mice after the transplantation of tumor, illustrating that the survival time of the scFv <HL5> administrated-group was remarkably prolonged.

**[0320]** Fig. 46 shows the survival time (days) of mice after the transplantation of tumor, illustrating that the survival time of the sc(Fv)<sub>2</sub> administrated-group was remarkably prolonged.

**[0321]** Fig. 47 is a scheme showing the method for constructing DNA fragment encoding the reconstructed 12B5 single chain Fv containing the linker sequence consisting of 15 amino acids and the structure thereof.

**[0322]** Fig. 48 shows the purification result of each 12B5 single chain Fv by gel filtration obtained in Example 7. 5 (1), illustrating that sc12B5 was divided into two peaks (fractions A and B).

[0323] Fig. 49 shows the analytical result of each fraction A and B by SDS-PAGE performed in Example 7. 5 (2).

[0324] Fig. 50 shows the analytical result of each fraction A and B by Superdex200 column performed in Example 7. 5 (2), illustrating that the major peak of fraction A was eluted at an apparent molecular weight of about 44 kD shown in (a) and that the major peak of fraction B was eluted at an apparent molecular weight of about 22kD shown in (b).

[0325] Fig. 51 shows the measurement result of the TPO-like agonist activity of sc12B5 and antibody 12B5 (IgG, Fab), illustrating that 12B5IgG and monovalent single chain Fv (sc12B5) showed TPO-like agonist activity in concentration-dependent manner.

[0326] Fig. 52 shows the measurement result of TOP-like agonist activity of sc12B5 monomer and dimer, illustrating that single chain Fv (sc12B5 dimer) having bivalent antigen-binding site had agonist activity about 400-fold higher than monovalent sc12B5 and that the efficacy is equivalent to or higher than human TPO.

[0327] Fig. 53 shows the purification result of obtained sc12E10 single chain antibody by gel filtration chromatography using Superdex200HR column, illustrating that 12E10sc3 was divided into two peaks (fractions A and B).

[0328] Fig. 54 shows the purification result of obtained db12E10 single chain antibody by gel filtration chromatography using Superdex200HR column, illustrating that 12E10sc3 was divided into two peaks (fractions C and D).

[0329] Fig. 55 shows SDS-PAGE analysis of fractions A and B (sc12E10 and fractions C and D (db12E10) under the reductive or non-reductive condition.

[0330] Fig. 56 shows the analytical result of fractions A and B by gel filtration chromatography using Superdex200HR column, illustrating (1) the major peak of fraction A was eluted at an apparent molecular weight of about 42 kD and (2) the major peak of fraction B was eluted at an apparent molecular weight of about 20kD.

[0331] Fig. 57 shows the analytical result of fractions C and D by gel filtration chromatography using Superdex200HR column, illustrating (1) the major peak of fraction C was eluted at an apparent molecular weight of about 69 kD and (2) the major peak of fraction B was eluted at an apparent molecular weight of about 41kD.

[0332] Fig. 58 is a graph showing the agonist activity of various 12E10 antibody molecules on MPL, illustrating that single chain Fvs (sc12E10 db12E10) showed TPO-like agonist activity while 12E10 IgG and 12E10 Fab did not.

[0333] Fig. 59 is a graph showing the agonist activity of monomer and dimer of sc12E10 and dimer and trimer of db12E10 on MPL, illustrating that dimer of sc12E10 and dimer and trimer of db12E10 showed higher TPO-like agonist activity than TPO.

## INDUSTRIAL APPLICABILITY

[0334] The modified antibodies of the invention have an agonist action capable of transducing a signal into cells by crosslinking a cell surface molecule(s) and are advantageous in that the permeability to tissues and tumors is high due to the lowered molecular size compared with antibody molecule (whole IgG). This invention provides the modified antibodies with an agonist activity remarkably higher than TPO or parent antibodies (whole IgG). Especially even parent antibodies without agonist activity can be altered into the modified antibodies with an agonist activity higher than TPO. Therefore the modified antibodies can be used as signal-transducing agonists. The modification of antibody molecule results in the reduction of side effects caused by intercellular crosslinking and provides novel medicines inducing only required action by crosslinking a cell surface molecule(s). Medical preparations containing as active ingredient the modified antibodies of the invention are useful as preventives and/or remedies for platelet-related-blood diseases, thrombocytopenia caused by chemotherapy for cancers or leukemia and the like.

## SEQUENCE LISTING

5

&lt;110&gt; CHUGAI SEIYAKU KABUSHIKI KAISHA

&lt;120&gt; Small remodeling agonist antibody against TPO

10

&lt;130&gt; FP1033

&lt;141&gt; 2001-10-22

15

&lt;150&gt; JP2000-321821

&lt;151&gt; 2000-10-20

&lt;150&gt; PCT/JP01/03288

20

&lt;151&gt; 2001-04-17

&lt;150&gt; JP2001-277314

25

&lt;151&gt; 2001-09-12

&lt;160&gt; 113

30

&lt;210&gt; 1

&lt;211&gt; 27

35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

40

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 1

45

ccatcctaatacgaactcactatagggc 27

50

&lt;210&gt; 2

&lt;211&gt; 27

&lt;212&gt; DNA

55

&lt;213&gt; Artificial Sequence

<220>

<223> PCR primer

<400> 2

ggatcccggg tggatggtgg gaagatg 27

<210> 3

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 3

ggatcccggg ccagtggata gacagatg 28

<210> 4

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 4

ggatcccggg agtggataga ccgatg 26

<210> 5

<211> 394

<212> DNA

<213> Mus

<220>

&lt;221&gt; CDS

&lt;222&gt; (1)... (393)

5 &lt;223&gt; pGEM-MiL. 1-57;signal peptide, 58-394;mature peptide

&lt;400&gt; 5

10 atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct gcg 48

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala

1 5 10 15

15 tcc agc agt gat gtt gtg atg acc caa act cca ctc tcc ctg cct gtc 96

Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val

20 20 25 30

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt 144

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu

25 35 40 45

cta cac agt aaa gga aac acc tat tta caa tgg tac cta cag aag cca 192

30 Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr Leu Gln Lys Pro

50 55 60

ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240

35 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser

65 70 75 80

40 ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca 288

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

85 90 95

45 ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc 336

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys

100 105 110

50 tct caa agt aca cat gtt ccg tac acg tcc gga ggg ggg acc aag ctg 384

Ser Gln Ser Thr His Val Pro Tyr Thr Ser Gly Gly Gly Thr Lys Leu

55 115 120 125

gaa ata aaa c

394

Glu Ile Lys

5

130

10

&lt;210&gt; 6

&lt;211&gt; 409

&lt;212&gt; DNA

15

&lt;213&gt; Mus

&lt;220&gt;

20

&lt;221&gt; CDS

&lt;222&gt; (1)... (408)

&lt;223&gt; pGEM-M1H. 1-57;signal peptide, 58-409;mature peptide

25

&lt;400&gt; 6

atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca ggt 48

30

Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly

1

5

10

15

gtc cac tcc cag gtc cag ctg cag cag tct gga cct gac ctg gta aag 96

35

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys

20

25

30

cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144

40

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35

40

45

gtt aac cat gtt atg cac tgg gtg aag cag aag cca ggg cag ggc ctt 192

45

Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu

50

55

60

gag tgg att gga tat att tat cct tac aat gat ggt act aag tac aat 240

50

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn

55

65

70

75

80

EP 1 327 680 A1

gag aag ttc aag ggc aag gcc aca ctg act tca gag aaa tcc tcc agc 288  
 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys Ser Ser Ser  
 5 85 90 95  
 gca gcc tac atg gag ctc agc agc ctg gcc tct gag gac tct gcg gtc 336  
 10 Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val  
 100 105 110  
 tac tac tgt gca aga ggg ggt tac tat agt tac gac gac tgg ggc caa 384  
 15 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln  
 115 120 125  
 20 gcc acc act ctc aca gtc tcc tca g 409  
 Gly Thr Thr Leu Thr Val Ser Ser  
 130 135  
 25  
 <210> 7  
 30 <211> 394  
 <212> DNA  
 <213> Mus  
 35 <220>  
 <221> CDS  
 40 <222> (1)... (393)  
 <223> pGEM-M2L. 1-57;signal peptide, 58-394;mature peptide  
 <400> 7  
 45 atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct ggt 48  
 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly  
 1 5 10 15  
 50 tcc agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc 96  
 Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val  
 55 20 25 30

agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt 144  
 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu  
 5                   35                   40                   45  
 gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag cca 192  
 Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro  
 10                   50                   55                   60  
 ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240  
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser  
 15                   65                   70                   75                   80  
 ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat ttc aca 288  
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr  
 20                   85                   90                   95  
 ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc 336  
 Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys  
 25                   100                   105                   110  
 tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg 384  
 Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu  
 30                   115                   120                   125  
 gaa ata aaa c 394  
 Glu Ile Lys  
 35                   130  
 40  
 45 <210> 8  
 <211> 409  
 <212> DNA  
 50 <213> Mus  
 <220>  
 55 <221> CDS

&lt;222&gt; (1)... (408)

&lt;223&gt; pGEM-M2H. 1-57;signal peptide, 58-409;mature peptide

&lt;400&gt; 8

5  
 atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca ggt 48  
 10 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly  
 1 5 10 15  
 gtc cac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag 96  
 15 Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
 20 cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144  
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 25 gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 192  
 Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu  
 30 gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 240  
 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn  
 35 gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 288  
 Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr  
 40 aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc 336  
 Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val  
 45 tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa 384  
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln  
 50 ggc acc act ctc aca gtc tcc tca g 409  
 55

Gly Thr Thr Leu Thr Val Ser Ser

130

135

5

<210> 9

10

<211> 32

<212> DNA

15

<213> Artificial Sequence

<220>

<223> PCR primer

20

<400> 9

cccaagcttc caccatgaag ttgcctgtta gg 32

25

<210> 10

<211> 32

30

<212> DNA

<213> Artificial Sequence

<220>

35

<223> PCR primer

<400> 10

40

cccaagcttc caccatggaa tggagctgga ta 32

45

<210> 11

<211> 34

<212> DNA

50

<213> Artificial Sequence

<220>

<223> PCR primer

55

<400> 11

cgcggatcca ctcacgtttt atttccagct tggt 34

5

<210> 12

<211> 34

10

<212> DNA

<213> Artificial Sequence

<220>

15

<223> PCR primer

<400> 12

20

cgcggatcca ctcacctgag gagactgtga gagt 34

25

<210> 13

<211> 30

<212> DNA

30

<213> Artificial Sequence

<220>

<223> PCR primer

35

<400> 13

catgccatgg cgcaggtcca gctgcagcag 30

40

<210> 14

<211> 27

45

<212> DNA

<213> Artificial Sequence

<220>

50

<223> PCR primer

<400> 14

55

accaccacct gaggagactg tgagagt 27

5  
 <210> 15  
 <211> 27  
 <212> DNA  
 10 <213> Artificial Sequence  
 <220>  
 <223> PCR primer  
 15 <400> 15  
 gtctcctcag gtggtggtgg ttcgggt 27  
 20  
 <210> 16  
 <211> 27  
 25 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 30 <223> PCR primer  
 <400> 16  
 35 cacaacatcc gatccgccac caccgga 27  
 40  
 <210> 17  
 <211> 27  
 <212> DNA  
 45 <213> Artificial Sequence  
 <220>  
 <223> PCR primer  
 50 <400> 17  
 ggcggatcgg atgttgtgat gacccaa 27  
 55

<210> 18

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 18

ccggaattct cattatttat cgtcatcgtc tttgtagtct tttatttcca gcttggt 57

<210> 19

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Linker amino acid sequence and nucleotide sequence

<400> 19

ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

5

10

15

<210> 20

<211> 828

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)... (822)

<223> pscM1. MABL1-scFv

&lt;400&gt; 20

5 atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc gct 48  
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
 1 5 10 15  
 10 gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga cct gac 96  
 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Asp  
 20 25 30  
 15 ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 144  
 Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly  
 20 35 40 45  
 tac acc ttc gtt aac cat gtt atg cac tgg gtg aag cag aag cca ggg 192  
 Tyr Thr Phe Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly  
 25 50 55 60  
 cag ggc ctt gag tgg att gga tat att tat cct tac aat gat ggt act 240  
 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr  
 30 65 70 75 80  
 aag tac aat gag aag ttc aag ggc aag gcc aca ctg act tca gag aaa 288  
 Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys  
 35 85 90 95  
 tcc tcc agc gca gcc tac atg gag ctc agc agc ctg gcc tct gag gac 336  
 Ser Ser Ser Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp  
 40 100 105 110  
 45 tct gcg gtc tac tac tgt gca aga ggg ggt tac tat agt tac gac gac 384  
 Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp  
 115 120 125  
 50 tgg ggc caa ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcg 432  
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser  
 55 130 135 140

ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gat gtt gtg atg acc caa 480  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln  
 5 145 150 155 160  
 act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 528  
 10 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser  
 165 170 175  
 tgc aga tct agt cag agc ctt cta cac agt aaa gga aac acc tat tta 576  
 15 Cys Arg Ser Ser Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu  
 180 185 190  
 caa tgg tac cta cag aag cca ggc cag tct cca aag ctc ctg atc tac 624  
 20 Gln Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr  
 195 200 205  
 25 aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt 672  
 Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
 30 210 215 220  
 gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag 720  
 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu  
 35 225 230 235 240  
 gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg 768  
 40 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr  
 245 250 255  
 tcc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac 816  
 45 Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp  
 260 265 270  
 50 gat aaa taatga 828  
 Asp Lys  
 55 <210> 21

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 21

acgcgtcgac tcccagggtcc agctgcagca g 31

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 22

gaaggtgtat ccagaagc 18

<210> 23

<211> 819

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)... (813)

<223> pCHOM1. MABL1-scFv

<400> 23

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

|    |   |     |     |     |  |
|----|---|-----|-----|-----|--|
|    | 1   | 5   | 10  | 15  |  |
| 5  | gtc gac tcc cag gtc cag ctg cag cag tct gga cct gac ctg gta aag 96  |     |     |     |  |
|    | Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys     |     |     |     |  |
|    | 20  | 25  | 30  |     |  |
| 10 | cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144 |     |     |     |  |
|    | Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe     |     |     |     |  |
|    | 35  | 40  | 45  |     |  |
| 15 | gtt aac cat gtt atg cac tgg gtg aag cag aag cca ggg cag ggc ctt 192 |     |     |     |  |
|    | Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu     |     |     |     |  |
| 20 | 50  | 55  | 60  |     |  |
|    | gag tgg att gga tat att tat cct tac aat gat ggt act aag tac aat 240 |     |     |     |  |
|    | Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn     |     |     |     |  |
| 25 | 65  | 70  | 75  | 80  |  |
|    | gag aag ttc aag ggc aag gcc aca ctg act tca gag aaa tcc tcc agc 288 |     |     |     |  |
| 30 | Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys Ser Ser Ser     |     |     |     |  |
|    | 85  | 90  | 95  |     |  |
| 35 | gca gcc tac atg gag ctc agc agc ctg gcc tct gag gac tct gcg gtc 336 |     |     |     |  |
|    | Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val     |     |     |     |  |
|    | 100   | 105 | 110 |     |  |
| 40 | tac tac tgt gca aga ggg ggt tac tat agt tac gac gac tgg ggc caa 384 |     |     |     |  |
|    | Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln     |     |     |     |  |
|    | 115   | 120 | 125 |     |  |
| 45 | ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt 432 |     |     |     |  |
|    | Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly     |     |     |     |  |
| 50 | 130   | 135 | 140 |     |  |
|    | ggg tcg ggt ggt ggc gga tcg gat gtt gtg atg acc caa act cca ctc 480 |     |     |     |  |
|    | Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu     |     |     |     |  |
| 55 | 145   | 150 | 155 | 160 |  |

EP 1 327 680 A1

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct 528  
 Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser  
 5 165 170 175  
 agt cag agc ctt cta cac agt aaa gga aac acc tat tta caa tgg tac 576  
 10 Ser Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr  
 180 185 190  
 cta cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc 624  
 15 Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser  
 195 200 205  
 aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg 672  
 20 Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly  
 210 215 220  
 aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga 720  
 25 Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly  
 225 230 235 240  
 gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg tcc gga ggg 768  
 30 Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Ser Gly Gly  
 245 250 255  
 ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat aaa taa 816  
 40 Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys  
 260 265 270  
 tga 819  
 45  
 <210> 24  
 <211> 828  
 50 <212> DNA  
 <213> Mus  
 55 <220>

&lt;221&gt; CDS

&lt;222&gt; (1)... (822)

&lt;223&gt; pscM2. MABL2-scFv

&lt;400&gt; 24

10 atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc gct 48  
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
 1 5 10 15  
 15 gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga cct gaa 96  
 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu  
 20 20 25 30  
 ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 144  
 Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly  
 25 35 40 45  
 tac acc ttc gct aac cat gtt att cac tgg gtg aag cag aag cca ggg 192  
 Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly  
 30 50 55 60  
 cag ggc ctt gag tgg att gga tat att tat cct tac aat gat ggt act 240  
 35 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr  
 65 70 75 80  
 40 aag tat aat gag aag ttc aag gac aag gcc act ctg act tca gac aaa 288  
 Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys  
 85 90 95  
 45 tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac 336  
 Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp  
 100 105 110  
 50 tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act tac gac gac 384  
 Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp  
 55 115 120 125

tgg ggc caa ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tgc 432  
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser  
 5           130                   135                   140  
 ggt ggt ggt ggt tgc ggt ggt ggc gga tgc gat gtt gtg atg acc caa 480  
 10 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln  
 145                   150                   155                   160  
 agt cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 528  
 15 Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser  
 165                   170                   175  
 tgc aga tca agt cag agc ctt gtg cac agt aat gga aag acc tat tta 576  
 20 Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr  
 180                   185                   190  
 cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac 624  
 25 His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr  
 195                   200                   205  
 aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt 672  
 30 Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
 210                   215                   220  
 gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct gag 720  
 40 Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu  
 225                   230                   235                   240  
 gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg 768  
 45 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr  
 245                   250                   255  
 ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac 816  
 50 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp  
 260                   265                   270  
 55 gat aaa taatga 828

Asp Lys

&lt;210&gt; 25

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Mus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)... (813)

&lt;223&gt; pCHOM2. MABL2-scFv

&lt;400&gt; 25

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag 96

Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys

20 25 30

cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35 40 45

gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 192

Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu

50 55 60

gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 240

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn

65 70 75 80

gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 288

Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr

|    |   |     |     |     |
|----|---|-----|-----|-----|
|    | 85  | 90  | 95  |     |
| 5  | aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc | 336 |     |     |
|    | Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val |     |     |     |
|    | 100   | 105 | 110 |     |
| 10 | tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa | 384 |     |     |
|    | Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln |     |     |     |
|    | 115   | 120 | 125 |     |
| 15 | ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt | 432 |     |     |
|    | Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly |     |     |     |
| 20 | 130   | 135 | 140 |     |
|    | ggt tcg ggt ggt ggc gga tcg gat gtt gtg atg acc caa agt cca ctc | 480 |     |     |
|    | Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu |     |     |     |
| 25 | 145   | 150 | 155 | 160 |
|    | tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca | 528 |     |     |
| 30 | Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser |     |     |     |
|    | 165   | 170 | 175 |     |
|    | agt cag agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac | 576 |     |     |
| 35 | Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr |     |     |     |
|    | 180   | 185 | 190 |     |
| 40 | ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc | 624 |     |     |
|    | Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser |     |     |     |
|    | 195   | 200 | 205 |     |
| 45 | aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg | 672 |     |     |
|    | Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val |     |     |     |
|    | 210   | 215 | 220 |     |
| 50 | aca gat ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga | 720 |     |     |
|    | Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly |     |     |     |
| 55 | 225   | 230 | 235 | 240 |

gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg 768  
 Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly  
 5 245 250 255  
 ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat aaa taa 816  
 10 Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys  
 260 265 270  
 tga 819  
 15  
 <210> 26  
 20 <211> 456  
 <212> DNA  
 <213> Mus  
 25 <220>  
 <221> CDS  
 30 <222> (1)... (450)  
 <223> pCHO-shIAP. Soluble human IAP  
 <400> 26  
 35 atg tgg ccc ctg gta gcg gcg ctg ttg ctg ggc tgc gcg tgc tgc gga 48  
 Met Trp Pro Leu Val Ala Ala Leu Leu Leu Gly Ser Ala Cys Cys Gly  
 40 1 5 10 15  
 tca gct cag cta cta ttt aat aaa aca aaa tct gta gaa ttc acg ttt 96  
 Ser Ala Gln Leu Leu Phe Asn Lys Thr Lys Ser Val Glu Phe Thr Phe  
 45 20 25 30  
 tgt aat gac act gtc gtc att cca tgc ttt gtt act aat atg gag gca 144  
 Cys Asn Asp Thr Val Val Ile Pro Cys Phe Val Thr Asn Met Glu Ala  
 50 35 40 45  
 caa aac act act gaa gta tac gta aag tgg aaa ttt aaa gga aga gat 192  
 55 Gln Asn Thr Thr Glu Val Tyr Val Lys Trp Lys Phe Lys Gly Arg Asp

|   |     |     |    |
|---|-----|-----|----|
| 50  | 55  | 60  |    |
| att tac acc ttt gat gga gct cta aac aag tcc act gtc ccc act gac   | 240 |     |    |
| Ile Tyr Thr Phe Asp Gly Ala Leu Asn Lys Ser Thr Val Pro Thr Asp   |     |     |    |
| 65  | 70  | 75  | 80 |
| ttt agt agt gca aaa att gaa gtc tca caa tta cta aaa gga gat gcc   | 288 |     |    |
| Phe Ser Ser Ala Lys Ile Glu Val Ser Gln Leu Leu Lys Gly Asp Ala   |     |     |    |
| 85  | 90  | 95  |    |
| tct ttg aag atg gat aag agt gat gct gtc tca cac aca gga aac tac   | 336 |     |    |
| Ser Leu Lys Met Asp Lys Ser Asp Ala Val Ser His Thr Gly Asn Tyr   |     |     |    |
| 100   | 105 | 110 |    |
| act tgt gaa gta aca gaa tta acc aga gaa ggt gaa acg atc atc gag   | 384 |     |    |
| Thr Cys Glu Val Thr Glu Leu Thr Arg Glu Gly Glu Thr Ile Ile Glu   |     |     |    |
| 115   | 120 | 125 |    |
| cta aaa tat cgt gtt gtt tca tgg ttt tct cca aat gaa aat gac tac   | 432 |     |    |
| Leu Lys Tyr Arg Val Val Ser Trp Phe Ser Pro Asn Glu Asn Asp Tyr   |     |     |    |
| 130   | 135 | 140 |    |
| aag gac gac gat gac aag tgatag  | 456 |     |    |
| Lys Asp Asp Asp Asp Lys   |     |     |    |
| 145   | 150 |     |    |
| <p>&lt;210&gt; 27</p> <p>&lt;211&gt; 46</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; Artificial Sequence</p> <p>&lt;220&gt;</p> <p>&lt;223&gt; PCR primer</p> <p>&lt;400&gt; 27</p> <p>ggaattccat atgcaagtgc aacttcaaca gtctggacct gaactg 46</p> |     |     |    |

<210> 28

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 28

ggaattctca ttattttatt tccagcttgg t 31

<210> 29

<211> 741

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)... (735)

<223> pscM2DEm02. MABL2-scFv

<400> 29

atg caa gtg caa ctt caa cag tct gga cct gaa ctg gta aag cct ggg 48

Met Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly

1 5 10 15

gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc gct aac 96

Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn

20 25 30

cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt gag tgg 144

His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp

35 40 45

att gga tat att tat cct tac aat gat ggt act aag tat aat gag aag 192  
 Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys  
 5                   50                   55                   60  
 ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc aca gcc 240  
 Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala  
 10                   65                   70                   75                   80  
 tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc tat tac 288  
 Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr  
 15                   85                   90                   95  
 tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa ggc acc 336  
 Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr  
 20                   100                   105                   110  
 act ctc aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg 384  
 Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 25                   115                   120                   125  
 ggt ggt ggc gga tcg gat gtt gtg atg acc caa agt cca ctc tcc ctg 432  
 Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu  
 30                   130                   135                   140  
 cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag 480  
 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln  
 35                   145                   150                   155                   160  
 agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag 528  
 Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln  
 40                   165                   170                   175  
 aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga 576  
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg  
 45                   180                   185                   190  
 ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat 624  
 50                   195                   200                   205  
 55

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp

195 200 205

ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat 672

Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr

210 215 220

ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc 720

Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr

225 230 235 240

aag ctg gaa ata aaa taatga 741

Lys Leu Glu Ile Lys

245

<210> 30

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 30

cagacagtgg ttcaaagt 18

<210> 31

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 31

cgcgctcgacc gatccgccac caccggaacc accaccaccc gaaccaccac caccttttat 60  
 ttccagcttg gt 72

<210> 32

<211> 1605

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)... (1599)

<223> pCHOM2(Fv)2. MABL2-sc(Fv)2

<400> 32

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag 96

Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys

20 25 30

cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35 40 45

gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 192

Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu

50 55 60

gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 240

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn

65 70 75 80

gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 288

|    |   |     |
|----|---|-----|
|    | Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr |     |
|    | 85 90 95  |     |
| 5  | aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc | 336 |
|    | Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val |     |
| 10 | 100 105 110   |     |
|    | tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa | 384 |
|    | Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln |     |
| 15 | 115 120 125   |     |
|    | ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt | 432 |
| 20 | Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly |     |
|    | 130 135 140   |     |
|    | ggg tcg ggt ggt ggc gga tcg gat gtt gtg atg acc caa agt cca ctc | 480 |
| 25 | Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu |     |
|    | 145 150 155 160   |     |
| 30 | tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca | 528 |
|    | Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser |     |
|    | 165 170 175   |     |
| 35 | agt cag agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac | 576 |
|    | Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr |     |
| 40 | 180 185 190   |     |
|    | ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc | 624 |
|    | Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser |     |
| 45 | 195 200 205   |     |
|    | aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg | 672 |
| 50 | Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val |     |
|    | 210 215 220   |     |
|    | aca gat ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga | 720 |
| 55 | Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly |     |

|    |   |      |     |     |  |
|----|---|------|-----|-----|--|
|    | 225   | 230  | 235 | 240 |  |
| 5  | ggt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg | 768  |     |     |  |
|    | Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly |      |     |     |  |
|    | 245   | 250  | 255 |     |  |
| 10 | ggg acc aag ctg gaa ata aaa ggt ggt ggt ggt tcg ggt ggt ggt ggt | 816  |     |     |  |
|    | Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly |      |     |     |  |
|    | 260   | 265  | 270 |     |  |
| 15 | tcg ggt ggt ggc gga tcg gtc gac tcc cag gtc cag ctg cag cag tct | 864  |     |     |  |
|    | Ser Gly Gly Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Gln Ser |      |     |     |  |
| 20 | 275   | 280  | 285 |     |  |
|    | gga cct gaa ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag | 912  |     |     |  |
|    | Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys |      |     |     |  |
| 25 | 290   | 295  | 300 |     |  |
|    | gct tct gga tac acc ttc gct aac cat gtt att cac tgg gtg aag cag | 960  |     |     |  |
| 30 | Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln |      |     |     |  |
|    | 305   | 310  | 315 | 320 |  |
|    | aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat | 1008 |     |     |  |
| 35 | Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn |      |     |     |  |
|    | 325   | 330  | 335 |     |  |
| 40 | gat ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act | 1056 |     |     |  |
|    | Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr |      |     |     |  |
|    | 340   | 345  | 350 |     |  |
| 45 | tca gac aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc | 1104 |     |     |  |
|    | Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala |      |     |     |  |
|    | 355   | 360  | 365 |     |  |
| 50 | tct gag gac tct ggc gtc tat tac tgt gca aga ggg ggt tac tat act | 1152 |     |     |  |
|    | Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr |      |     |     |  |
| 55 | 370   | 375  | 380 |     |  |

EP 1 327 680 A1

5      tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc tca ggt ggt 1200  
 Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly  
 385                      390                      395                      400  
 10      ggt ggt tgc ggt ggt ggt ggt tgc ggt ggt ggc gga tgc gat gtt gtg 1248  
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val  
                          405                      410                      415  
 15      atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc 1296  
 Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala  
                          420                      425                      430  
 20      tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt aat gga aag 1344  
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys  
                          435                      440                      445  
 25      acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctc 1392  
 Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu  
                          450                      455                      460  
 30      ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc 1440  
 Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe  
 35      465                      470                      475                      480  
 agt ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg 1488  
 Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val  
 40      485                      490                      495  
 gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt 1536  
 45      Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val  
                          500                      505                      510  
 50      ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa 1584  
 Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys  
                          515                      520                      525  
 55      gac gat gac gat aaa taatga 1605

Asp Asp Asp Asp Lys

530

5

<210> 33

10

<211> 23

<212> DNA

<213> Artificial Sequence

15

<220>

<223> PCR primer

20

<400> 33

tgaggaattc ccaccatggg atg 33

25

<210> 34

<211> 40

<212> DNA

30

<213> Artificial Sequence

<220>

35

<223> PCR primer

<400> 34

cacgacgtca ctcgagactg tgagagtggg gccttgcccc 40

40

<210> 35

45

<211> 40

<212> DNA

<213> Artificial Sequence

50

<220>

<223> PCR primer

55

<400> 35

agtctcgagt gacgtcgtga tgacccaaag tccactctcc 40

5

<210> 36

<211> 31

10

<212> DNA

<213> Artificial Sequence

<220>

15

<223> PCR primer

<400> 36

20

gactggatcc tcattattta tcgtcatcgt c 31

<210> 37

25

<211> 22

<212> DNA

<213> Artificial Sequence

30

<220>

<223> PCR primer

35

<400> 37

cgcgtaatac gactcactat ag 22

40

<210> 38

<211> 46

45

<212> DNA

<213> Artificial Sequence

<220>

50

<223> PCR primer

<400> 38

55

gcaattggac ctgttttata tcgagcttgg tccccctcc gaacgt 46

<210> 39

5 <211> 45

<212> DNA

10 <213> Artificial Sequence

<220>

<223> PCR primer

15 <400> 39

gctcgagata aaacaggtcc aattgcagca gtctggacct gaact 45

20 <210> 40

<211> 60

25 <212> DNA

<213> Artificial Sequence

<220>

30 <223> PCR primer

<400> 40

35 gactggatcc tcattattta tcgtcatcgt cttttagtc tgaggagact gtgagagtgg 60

<210> 41

40 <211> 32

<212> DNA

45 <213> Artificial Sequence

<220>

<223> PCR primer

50 <400> 41

gactgaattc ccaccatgaa gttgcctgtt ag 32

55

<210> 42

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 42

cagtctcgag tgggtggtcc gacgtcgtga tgacccaaag 40

<210> 43

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 43

cagtctcgag tgggtggtgt tccgacgtcg tgatgaccca aag 43

<210> 44

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 44

cagtctcgag tgggtggtgt ggtccgacg tcgtgatgac ccaaag 46

<210> 45

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 45

cagtctcgag tgggtggtggt ggtggttccg acgtcgtgat gacccaaag 49

<210> 46

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 46

cagtctcgag tgggtggtggt ggtggtggtt ccgacgtcgt gatgacccaa ag 52

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 47

ggccgcatgt tgtcacgaat 20

<210> 48

<211> 780

&lt;212&gt; DNA

&lt;213&gt; Mus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)... (768)

&lt;223&gt; CF2HL-0/pCOS1. MABL2-scFv&lt;HL-0&gt;

&lt;400&gt; 48

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt gtc 51

MET Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val

gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag cct ggg 102

Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly

gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc gct aac cat 153

Ala Ser Val Lys MET Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn His

gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt gag tgg att gga 204

Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly

tat att tat cct tac aat gat ggt act aag tat aat gag aag ttc aag gac 255

Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp

aag gcc act ctg act tca gac aaa tcc tcc acc aca gcc tac atg gac ctc 306

Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala Tyr MET Asp Leu

agc agc ctg gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt 357

Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly

tac tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcg agt 408  
 Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser  
 5 120 125 130 135  
 gac gtc gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga gat 459  
 10 Asp Val Val MET Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp  
 140 145 150  
 caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt aat gga 510  
 15 Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly  
 155 160 165 170  
 aag acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctc 561  
 20 Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu  
 175 180 185  
 ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt 612  
 25 Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser  
 190 195 200  
 ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct 663  
 Gly Ser Gly Ser Val Thr Asp Phe Thr Leu MET Ile Ser Arg Val Glu Ala  
 35 205 210 215 220  
 gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg 714  
 40 Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr  
 225 230 235  
 ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat 765  
 45 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp  
 240 245 250 255  
 aaa taa tga gga tcc 780  
 50 Lys

55 <210> 49

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 49

caagctcgag ataaaatccg gaggccaggt ccaattgcag cagtc 45

<210> 50

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 50

caagctcgag ataaaatccg gaggtggcca ggtccaattg cagcagtc 48

<210> 51

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 51

caagctcgag ataaaatccg gaggtggtgg ccaggtccaa ttgcagcagt c 51

<210> 52

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 52

caagctcgag ataaaatccg gaggtggtgg tggccaggtc caattgcagc agtc 54

<210> 53

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 53

caagctcgag ataaaatccg gaggtggtgg tggcggccag gtccaattgc agcagtc 57

<210> 54

<211> 780

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)... (768)

<223> CF2LH-0/pCOS1. MABL2-scFv<LH-0>

<400> 54

atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct ggt tcc 51

MET Lys Leu Pro Val Arg Leu Leu Val Leu MET Phe Trp Ile Pro Gly Ser

5

10

15

agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt 102  
 Ser Ser Asp Val Val MET Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu  
 5                   20                   25                   30  
 gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt 153  
 10 Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser  
                   35                   40                   45                   50  
 aat gga aag acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca 204  
 15 Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro  
                   55                   60                   65  
 aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg 255  
 20 Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg  
                   70                   75                   80                   85  
 ttc agt ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg 306  
 25 Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu MET Ile Ser Arg Val  
                   90                   95                   100  
 gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg 357  
 30 Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro  
                   105                   110                   115  
 tac acg ttc gga ggg ggg acc aag ctc gag ata aaa cag gtc caa ttg cag 408  
 35 Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gln Val Gln Leu Gln  
                   120                   125                   130                   135  
 cag tct gga cct gaa ctg gta aag cct ggg gct tca gtg aag atg tcc tgc 459  
 40 Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys MET Ser Cys  
                   140                   145                   150  
 aag gct tct gga tac acc ttc gct aac cat gtt att cac tgg gtg aag cag 510  
 45 Lys Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln  
                   155                   160                   165                   170  
 aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 561  
 55

Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp  
 175 180 185  
 5 ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act tca gac 612  
 Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp  
 10 190 195 200  
 aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac 663  
 Lys Ser Ser Thr Thr Ala Tyr MET Asp Leu Ser Ser Leu Ala Ser Glu Asp  
 15 205 210 215 220  
 tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg 714  
 20 Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp  
 225 230 235  
 ggc caa ggc acc act ctc aca gtc tcc tca gac tac aaa gac gat gac gat 765  
 25 Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Asp Tyr Lys Asp Asp Asp Asp  
 240 245 250 255  
 30 aaa taa tga gga tcc 780  
 Lys  
 35 <210> 55  
 <211> 351  
 40 <212> DNA  
 <213> Human  
 <220>  
 45 <221> CDS  
 <222> (1)... (351)  
 <223> 12B5HV. 1-351 peptide  
 50 <400> 55  
 cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cgg ccc ggg ggg 48  
 55 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|    | 1   | 5   | 10  | 15  |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 5  | tcc | ctg | agt | ctc | tcc | tgt | gca | gtc | tct | gga | atc | acc | ctc | agg | acc | tac | 96  |
|    | Ser | Leu | Ser | Leu | Ser | Cys | Ala | Val | Ser | Gly | Ile | Thr | Leu | Arg | Thr | Tyr |     |
|    |     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |     |
| 10 | ggc | atg | cac | tgg | gtc | cgc | cag | gct | cca | ggc | aag | ggg | ctg | gag | tgg | gtg | 144 |
|    | Gly | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |     |
|    |     | 35  |     | 40  |     | 45  |     |     |     |     |     |     |     |     |     |     |     |
| 15 | gca | ggt | ata | tcc | ttt | gac | gga | aga | agt | gaa | tac | tat | gca | gac | tcc | gtg | 192 |
|    | Ala | Gly | Ile | Ser | Phe | Asp | Gly | Arg | Ser | Glu | Tyr | Tyr | Ala | Asp | Ser | Val |     |
| 20 |     | 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
|    | cag | ggc | cga | ttc | acc | atc | tcc | aga | gac | agt | tcc | aag | aac | acc | ctg | tat | 240 |
|    | Gln | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Ser | Ser | Lys | Asn | Thr | Leu | Tyr |     |
| 25 |     | 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
|    | ctg | caa | atg | aac | agc | ctg | aga | gcc | gag | gac | acg | gct | gtg | tat | tac | tgt | 288 |
| 30 | Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |     |
|    |     | 85  |     | 90  |     | 95  |     |     |     |     |     |     |     |     |     |     |     |
| 35 | gcg | aga | gga | gca | cat | tat | ggt | ttc | gat | atc | tgg | ggc | caa | ggg | aca | atg | 336 |
|    | Ala | Arg | Gly | Ala | His | Tyr | Gly | Phe | Asp | Ile | Trp | Gly | Gln | Gly | Thr | Met |     |
|    |     | 100 |     | 105 |     | 110 |     |     |     |     |     |     |     |     |     |     |     |
| 40 | gtc | acc | gtc | tcg | agt |     |     |     |     |     |     |     |     |     |     |     | 351 |
|    | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |     |

115

&lt;210&gt; 56

&lt;211&gt; 57

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;220&gt;

<221> CDS

<222> (1)... (57)

<223> reader sequence

<400> 56

atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt tta aga ggt 48

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly

5

10

15

gtc cag tgt

57

Val Gln Cys

<210> 57

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-1

<400> 57

atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60

gtgcagctgg tgcagtctgg gggaggcttg gtccggcccg gggggtcctt gagtc 115

<210> 58

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-2

<400> 58

aaggatatac ctgccaccca ctccagcccc ttgcctggag cctggcggac ccagtgcattg 60  
ccgtaggtcc tgagggtgat tccagagact gcacaggaga gactcaggga ccccc 115

<210> 59

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-3

<400> 59

ggcaggtata tcctttgacg gaagaagtga atactatgca gactccgtgc agggccgatt 60  
caccatctcc agagacagtt ccaagaacac cctgtatctg caaatgaaca gcctg 115

<210> 60

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-4

<400> 60

actcgagacg gtgaccattg tcccttgccc ccagatatcg aaaccataat gtgctcctct 60  
cgcacagtaa tacacagccg tgcctcggc tctcaggctg ttcatttg 108

<210> 61

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-S, PCR primer

<400> 61

ttcaagcttc caccatggag tttagggctga gc 32

<210> 62

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-A, PCR primer

<400> 62

ttgggatcca ctcaccactc gagacgggtga ccat 34

<210> 63

<211> 588

<212> DNA

<213> Human

<220>

<221> CDS

<222> (236)... (558)

<223> 1-235;intron, 236-558;Human IgG constant region (partial)

<400> 63

gaattcgtga gtggatccca agctagcttt ctggggcagg ccaggcctga ctttggttt 60

ggggcaggga gggggctaag gtgaggcagg tggcgccagc caggtgcaca cccaatgcc 120

atgagcccag aacttgacg ctgaacctcg cggacagtta agaaccagg ggcctctgcg 180

ccctgggccc agctctgtcc cacaccggg tcacatggca caacctctct tgca gcc 237

Ala

1

tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc 285  
 5 Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser  
                     5                    10                    15  
 acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc 333  
 10 Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe  
                     20                    25                    30  
 ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc 381  
 15 Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly  
                     35                    40                    45  
 gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc 429  
 20 Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
                     50                    55                    60                    65  
 agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac 477  
 25 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr  
                     70                    75                    80  
 atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa 525  
 35 Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys  
                     85                    90                    95  
 gtt gag ccc aaa tct tgt gac aaa act cac aca 558  
 40 Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
                     100                    105  
 45 <210> 64  
       <211> 27  
 50 <212> DNA  
       <213> Artificial Sequence  
       <220>  
 55 <223> G1CH1-S, PCR primer

<400> 64

tgagaattcg tgagtggatc ccaagct 27

<210> 65

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> G1CH1-A, PCR primer

<400> 65

aaaagatcctt tatcatgtgt gagttttgtc acaagatttg ggctcaactt tcttgtccac 60

<210> 66

<211> 432

<212> DNA

<213> Human

<220>

<221> CDS

<222> (12)... (419)

<223> HEF-12B5H-g gamma. 12-419 peptide

<400> 66

aagcttccac c atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt 50

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu

1

5

10

tta aga ggt gtc cag tgt cag gtg cag ctg gtg cag tct ggg gga ggc 98

Leu Arg Gly Val Gln Cys Gln Val Gln Leu Val Gln Ser Gly Gly Gly

15

20

25

ttg gtc cgg ccc ggg ggg tcc ctg agt ctc tcc tgt gca gtc tct gga 146

Leu Val Arg Pro Gly Gly Ser Leu Ser Leu Ser Cys Ala Val Ser Gly  
 30 35 40 45  
 5 atc acc ctc agg acc tac ggc atg cac tgg gtc cgc cag gct cca ggc 194  
 Ile Thr Leu Arg Thr Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly  
 10 50 55 60  
 aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga agt gaa 242  
 15 Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg Ser Glu  
 65 70 75  
 tac tat gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt 290  
 20 Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser  
 80 85 90  
 tcc aag aac acc ctg tat ctg caa atg aac agc ctg aga gcc gag gac 338  
 25 Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
 95 100 105  
 30 acg gct gtg tat tac tgt gcg aga gga gca cat tat ggt ttc gat atc 386  
 Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ala His Tyr Gly Phe Asp Ile  
 110 115 120 125  
 35 tgg ggc caa ggg aca atg gtc acc gtc tcg agt ggtgagtgga tcc 432  
 Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser  
 40 130 135

45 <210> 67

<211> 321

<212> DNA

50 <213> Human

<220>

<221> CDS

55 <222> (1)... (321)

<223> 12B5LV. 1-321 peptide

<400> 67

gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct att gga 48

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly

1 5 10 15

gac aga gtc acc atc acc tgc cgg gcc agc gag ggt att tat cac tgg 96

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp

20 25 30

ttg gcc tgg tat cag cag aag cca ggg aaa gcc cct aaa ctc ctg atc 144

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

tat aag gcc tct agt tta gcc agt ggg gcc cca tca agg ttc agc ggc 192

Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly

50 55 60

agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

gat gat ttt gca act tat tac tgc caa caa tat agt aat tat ccg ctc 288

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu

85 90 95

act ttc ggc gga ggg acc aag ctg gag atc aaa 321

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 68

<211> 66

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)... (66)

<223> reader sequence

<400> 68

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48

MET Asp MET Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp

5

10

15

ctc cca ggt gcc aaa tgt

66

Leu Pro Gly Ala Lys Cys

20

<210> 69

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-1

<400> 69

atggacatga gggccccgc tcagctcctg gggctcctgc tgctctggct cccaggtgcc 60

aaatgtgaca tccagatgac ccagtctcct tccacctgt ctgcatctat 110

<210> 70

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-2

<400> 70

5 ggagtttagg ggctttccct ggcttctgct gataccaggc caaccagtga taaataccct 60  
cgctggcccg gcaggtgatg gtgactctgt ctccaataga tgcagacagg 110

10 <210> 71

<211> 110

15 <212> DNA

<213> Artificial Sequence

<220>

20 <223> 12B5VL-3

<400> 71

25 aagcccctaa actcctgac tataaggcct ctagtttagc cagtggggcc ccatcaaggt 60  
tcagcggcag tggatctggg acagatttca ctctaccat cagcagcctg 110

30 <210> 72

<211> 103

35 <212> DNA

<213> Artificial Sequence

<220>

40 <223> 12B5VL-4

<400> 72

45 tttgatctcc agcttggtcc ctccgccgaa agtgagcgga taattactat attgttgga 60  
gtaataagtt gcaaaatcat caggctgcag gctgctgatg gtg 103

50 <210> 73

<211> 32

55 <212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-S; PCR primer

<400> 73

ttcaagcttc caccatggac atgagggtcc cc 32

<210> 74

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-A, PCR primer

<400> 74

tctaggatcc actcacgttt gatctccagc ttggt 35

<210> 75

<211> 415

<212> DNA

<213> Human

<220>

<221> CDS

<222> (12)... (398)

<223> HEF-12B5H-g kappa. 12-398 peptide

<400> 75

aagcttcac c atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg 50

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu

1

5

10

ctg ctc tgg ctc cca ggt gcc aaa tgt gac atc cag atg acc cag tct 98

Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser

|    |   |     |     |     |
|----|---|-----|-----|-----|
|    | 15  | 20  | 25  |     |
| 5  | cct tcc acc ctg tct gca tct att gga gac aga gtc acc atc acc tgc | 146 |     |     |
|    | Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys |     |     |     |
|    | 30  | 35  | 40  | 45  |
| 10 | cgg gcc agc gag ggt att tat cac tgg ttg gcc tgg tat cag cag aag | 194 |     |     |
|    | Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys |     |     |     |
|    | 50  | 55  | 60  |     |
| 15 | cca ggg aaa gcc cct aaa ctc ctg atc tat aag gcc tct agt tta gcc | 242 |     |     |
|    | Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala |     |     |     |
| 20 | 65  | 70  | 75  |     |
|    | agt ggg gcc cca tca agg ttc agc ggc agt gga tct ggg aca gat ttc | 290 |     |     |
|    | Ser Gly Ala Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe |     |     |     |
| 25 | 80  | 85  | 90  |     |
|    | act ctc acc atc agc agc ctg cag cct gat gat ttt gca act tat tac | 338 |     |     |
| 30 | Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr |     |     |     |
|    | 95  | 100 | 105 |     |
|    | tgc caa caa tat agt aat tat ccg ctc act ttc ggc gga ggg acc aag | 386 |     |     |
| 35 | Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys |     |     |     |
|    | 110   | 115 | 120 | 125 |
| 40 | ctg gag atc aaa cgtgagtgga tcttaga                              | 415 |     |     |
|    | Leu Glu Ile Lys   |     |     |     |

45                   <210> 76  
                  <211> 24  
50                   <212> DNA  
                  <213> Artificial Sequence  
                  <220>  
55                   <223> FLAG tag sequence

<400> 76

gac tac aag gat gac gac gat aag 24

Asp Tyr Lys Asp Asp Asp Asp Lys

5

<210> 77

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5-S, PCR primer

<400> 77

atagaattcc accatggagt ttgggctgag c 31

<210> 78

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> HuVHJ3, PCR primer

<400> 78

tgaagagacg gtgaccattg tccc 24

<210> 79

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

5                   <223> RhuJH3, PCR primer  
                   <400> 79  
                   ggacaatggc caccgtctct tcaggtgg 28  
  
 10                  <210> 80  
                   <211> 32  
                   <212> DNA  
 15                  <213> Artificial Sequence  
                   <220>  
 20                  <223> RhuVK1, PCR primer  
                   <400> 80  
                   ggagactggg tcactctggat gtccgatccg cc 32  
 25  
  
                   <210> 81  
 30                  <211> 23  
                   <212> DNA  
                   <213> Artificial Sequence  
 35                  <220>  
                   <223> HuVK1.2, PCR primer  
 40                  <400> 81  
                   gacatccaga tgaccagtc tcc 23  
  
 45                  <210> 82  
                   <211> 59  
                   <212> DNA  
 50                  <213> Artificial Sequence  
                   <220>  
 55                  <223> 12B5F-A, PCR primer

<400> 82

attgcggccg cttatcactt atcgctgtca tccttgtagt ctttgatctc cagcttggt 59

<210> 83

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Linker amino acid sequence and nucleotide sequence

<400> 83

ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

5

10

15

<210> 84

<211> 823

<212> DNA

<213> Human

<220>

<221> CDS

<222> (12)... (809)

<223> sc12B5, Single chain Fv

<400> 84

aagcttccac c atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt 50

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu

1

5

10

tta aga ggt gtc cag tgt cag gtg cag ctg gtg cag tct ggg gga ggc 98

Leu Arg Gly Val Gln Cys Gln Val Gln Leu Val Gln Ser Gly Gly Gly

|    |   |     |     |     |
|----|---|-----|-----|-----|
|    | 15  | 20  | 25  |     |
| 5  | ttg gtc cgg ccc ggg ggg tcc ctg agt ctc tcc tgt gca gtc tct gga | 146 |     |     |
|    | Leu Val Arg Pro Gly Gly Ser Leu Ser Leu Ser Cys Ala Val Ser Gly |     |     |     |
|    | 30  | 35  | 40  | 45  |
| 10 | atc acc ctc agg acc tac ggc atg cac tgg gtc cgc cag gct cca ggc | 194 |     |     |
|    | Ile Thr Leu Arg Thr Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly |     |     |     |
|    | 50  | 55  | 60  |     |
| 15 | aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga agt gaa | 242 |     |     |
|    | Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg Ser Glu |     |     |     |
| 20 | 65  | 70  | 75  |     |
|    | tac tat gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt | 290 |     |     |
|    | Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser |     |     |     |
| 25 | 80  | 85  | 90  |     |
|    | tcc aag aac acc ctg tat ctg caa atg aac agc ctg aga gcc gag gac | 338 |     |     |
| 30 | Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp |     |     |     |
|    | 95  | 100 | 105 |     |
| 35 | acg gct gtg tat tac tgt gcg aga gga gca cat tat ggt ttc gat atc | 386 |     |     |
|    | Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ala His Tyr Gly Phe Asp Ile |     |     |     |
|    | 110   | 115 | 120 | 125 |
| 40 | tgg ggc caa ggg aca atg gtc acc gtc tcg agt ggt ggt ggt ggt tcg | 434 |     |     |
|    | Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser |     |     |     |
|    | 130   | 135 | 140 |     |
| 45 | ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag | 482 |     |     |
|    | Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln |     |     |     |
|    | 145   | 150 | 155 |     |
| 50 | tct cct tcc acc ctg tct gca tct att gga gac aga gtc acc atc acc | 530 |     |     |
|    | Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr |     |     |     |
| 55 | 160   | 165 | 170 |     |



Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Ser Tyr  
 20 25 30  
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60  
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Ser Gln Phe Ser Leu  
 65 70 75 80  
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 Arg Gly Arg Tyr Phe Asp Val Trp Gly Arg Gly Thr Met Val Thr Val  
 100 105 110  
 Ser Ser  
 <210> 86  
 <211> 342  
 <212> DNA  
 <213> Human  
 <400> 86  
 caggtgcagc tgcagcagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
 acctgcactg tctctggtga ctccatcagt agttactact ggagctggat tcggcagccc 120  
 ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180  
 ccctccctca agagtcgagt caccatatca gtagacacgt ccaagagcca gttctccctg 240  
 aagctgagct ctgtgaccgc cgcagacacg gccgtgtatt actgtgcgag agggcggtac 300  
 ttcgatgtct ggggcggtgg caccatggtc actgtctcct ca 342  
 <210> 87

<211> 57

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)... (57)

<223> reader sequence

<308> GenBank No. AF062252

<400> 87

atg aaa cat ctg tgg ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg 48

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1

5

10

15

gtc ctg tcc

57

Val Leu Ser

<210> 88

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10VH1

<400> 88

atgaaacatc tgtggttctt cttctcctg gtggcagctc ccagatgggt cctgtcccag 60

gtgcagctgc agcagtcggg cccaggactg gtgaagcctt cggagaccct 110

<210> 89

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10VH2

<400> 89

acccaatcca ctccagtcctc ttccctgggg gctgccgaat ccagctccag tagtaactac 60  
tgatggagtc accagagaca gtgcagggtga gggacagggt ctccgaaggc 110

<210> 90

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10VH3

<400> 90

tggagtggat tgggtatata tattacagtg ggagcaccaa ctacaacccc tccctcaaga 60  
gtcgagtcac catatcagta gacacgtcca agagccagtt ctccctgaag 110

<210> 91

<211> 114

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10VH4

<400> 91

tgaggagaca gtgaccatgg tgccacggcc ccagacatcg aagtaccgcc ctctgcaca 60  
gtaatacacg gccgtgtctg cggcgggtcac agagctcagc ttcagggaga actg 114

<210> 92

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10VHS, PCR primer

<400> 92

ttcaagcttc caccatgaaa catctgtggt tc 32

<210> 93

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10VHA, PCR primer

<400> 93

ttgggatcca ctcacctgag gagacagtga ccat 34

<210> 94

<211> 426

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (12)... (417)

<223> 12E10H, H chain V region

<400> 94

aagcttcac c atg aaa cat ctg tgg ttc ttc ctt ctc ctg gtg gca gct 50

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala

1 5 10  
 5 ccc aga tgg gtc ctg tcc cag gtg cag ctg cag cag tcg ggc cca gga 98  
 Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Gly  
 15 20 25  
 10 ctg gtg aag cct tcg gag acc ctg tcc ctc acc tgc act gtc tct ggt 146  
 Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
 30 35 40 45  
 15 gac tcc atc agt agt tac tac tgg agc tgg att cgg cag ccc cca ggg 194  
 Asp Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly  
 20 50 55 60  
 aag gga ctg gag tgg att ggg tat atc tat tac agt ggg agc acc aac 242  
 Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn  
 25 65 70 75  
 tac aac ccc tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc 290  
 Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser  
 30 80 85 90  
 aag agc cag ttc tcc ctg aag ctg agc tct gtg acc gcc gca gac acg 338  
 Lys Ser Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
 95 100 105  
 40 gcc gtg tat tac tgt gcg aga ggg cgg tac ttc gat gtc tgg ggc cgt 386  
 Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Phe Asp Val Trp Gly Arg  
 110 115 120 125  
 45 ggc acc atg gtc act gtc tcc tca ggtgagtgga tcccaa 426  
 Gly Thr Met Val Thr Val Ser Ser

130

&lt;210&gt; 95

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Mus

&lt;400&gt; 95

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ser Pro Gly Gln

1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr

20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu

35 40 45

Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe

50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Thr Arg

85 90 95

Ser Thr Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105 110

&lt;210&gt; 96

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Mus

&lt;400&gt; 96

tcctatgtgc tgactcagcc accctcggtg tcagggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag 120

caccagga aagccccaa actcatgatt tatgaggga gtaaaggcc ctcagggtt 180

tctaategct tctctggctc caagtctggc aacacggcct ccctgacat ctctgggctc 240  
 caggctgagg acgaggctga ttattactgc agctcatata caaccagaag cactcgggtg 300  
 ttcggcggag ggaccaagct gaccgtccta 330

<210> 97

<211> 57

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)... (57)

<223> reader sequence

<310>

<400> 97

atg gcc tgg acc gtt ctc ctc ctc ggc ctc ctc tct cac tgc aca ggc 48

Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly

1 5 10 15

tct gtg acc 57

Ser Val Thr

<210> 98

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10VL1, PCR primer

<400> 98

atggcctgga ccgttctcct cctcggcctc ctctctcact gcacaggctc tgtgacctcc 60

tatgtgctga ctcagccacc ctcgggtgtca gggctctctg gacagtcgat 110

5

<210> 99

<211> 62

10

<212> DNA

<213> Artificial Sequence

<220>

15

<223> 12E10VL2, PCR primer

<400> 99

20

tcatgagttt gggggctttg cctgggtgct gttggtacca ggagacatag ttataaccac 60

caacgtcact gctggttcca gtgcaggaga tggatgatga ctgtccagga 110

25

<210> 100

<211> 110

30

<212> DNA

<213> Artificial Sequence

<220>

35

<223> 12E10VL3, PCR primer

<400> 100

40

ccccaaact catgatttat gagggcagta aacggcctc aggggtttct aatcgcttct 60

ctggctccaa gtctggcaac acggcctccc tgaccatctc tgggtccag 110

45

<210> 101

<211> 102

50

<212> DNA

<213> Artificial Sequence

<220>

55

<223> 12E10VL4, PCR primer

<400> 101

taggacggtc agcttgggtcc ctccgccgaa caccgcgagtg cttctgggtg tatatgagct 60  
gcagtaataa tcagcctcgt cctcagcctg gagccagag at 102

<210> 102

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10VLS, PCR primer

<400> 102

atcaagcttc caccatggcc tggaccgttc t 31

<210> 103

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10VLA, PCR primer

<400> 103

ctaggatccg ggctgaccta ggacggtcag cttggt 36

<210> 104

<211> 387

<212> DNA

<213> Mus

<220>

<221> CDS

&lt;222&gt; (1)... (387)

&lt;223&gt; 12E10L, L chain V region

&lt;310&gt;

&lt;400&gt; 104

5  
 10 atg gcc tgg acc gtt ctc ctc ctc ggc ctc ctc tct cac tgc aca ggc 48  
 Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly  
 1 5 10 15  
 15 tct gtg acc tcc tat gtg ctg act cag cca ccc tcg gtg tca ggg tct 96  
 Ser Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ser  
 20 20 25 30  
 cct gga cag tcg atc acc atc tcc tgc act gga acc agc agt gac gtt 144  
 Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val  
 25 35 40 45  
 ggt ggt tat aac tat gtc tcc tgg tac caa cag cac cca ggc aaa gcc 192  
 Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala  
 30 50 55 60  
 ccc aaa ctc atg att tat gag ggc agt aaa cgg ccc tca ggg gtt tct 240  
 Pro Lys Leu Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser  
 35 65 70 75 80  
 40 aat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc 288  
 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile  
 85 90 95  
 45 tct ggg ctc cag gct gag gac gag gct gat tat tac tgc agc tca tat 336  
 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr  
 100 105 110  
 50 Aca acc aga agc act cgg gtg ttc ggc gga ggg acc aag ctg acc gtc 384  
 Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val  
 55 115 120 125

cta

387

Leu

5

&lt;210&gt; 105

10

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

15

&lt;220&gt;

&lt;221&gt; CDS

20

&lt;222&gt; (1)... (24)

&lt;223&gt; FLAG, reader sequence

&lt;400&gt; 105

25

gac tac aag gat gac gac gat aag 24

Asp Tyr Lys Asp Asp Asp Asp Lys

30

&lt;210&gt; 106

&lt;211&gt; 30

35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

40

&lt;223&gt; 12E10S, PCR primer

&lt;400&gt; 106

45

tatgaattcc accatgaaac atctgtggtt 30

&lt;210&gt; 107

50

&lt;211&gt; 38

&lt;212&gt; DNA

55

&lt;213&gt; Artificial Sequence

<220>

<223> DB2, PCR primer

<400> 107

taggagctac cgcctccacc tgaggagaca gtgaccat 38

<210> 108

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> DB1, PCR primer

<400> 108

gtctcctcag gtggaggcgg tagctcctat gtgtgactc agcc 44

<210> 109

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> 12E10FA, PCR primer

<400> 109

attgcggccg cttatcactt atcgtcgtca tccttgtagt ctaggacggt cagcttggt 59

<210> 110

<211> 792

<212> DNA

<213> Artificial Sequence

<220>

&lt;221&gt; CDS

&lt;222&gt; (11)... (778)

&lt;223&gt; 12E10, Single chain Fv

&lt;400&gt; 110

10 gaattccacc atg aaa cat ctg tgg ttc ttc ctt ctc ctg gtg gca gct 49  
     Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala  
         1                    5                    10

15 ccc aga tgg gtc ctg tcc cag gtg cag ctg cag cag tcg ggc cca gga 97  
     Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Gly  
         15                    20                    25

20 ctg gtg aag cct tcg gag acc ctg tcc ctc acc tgc act gtc tct ggt 145  
     Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
         30                    35                    40                    45

25 gac tcc atc agt agt tac tac tgg agc tgg att cgg cag ccc cca ggg 193  
     Asp Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly  
         50                    55                    60

30 aag gga ctg gag tgg att ggg tat atc tat tac agt ggg agc acc aac 241  
     Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn  
         65                    70                    75

35 tac aac ccc tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc 289  
     Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser  
         80                    85                    90

40 aag agc cag ttc tcc ctg aag ctg agc tct gtg acc gcc gca gac acg 337  
     Lys Ser Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
         95                    100                    105

45 gcc gtg tat tac tgt gcg aga ggg cgg tac ttc gat gtc tgg ggc cgt 385  
     Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Phe Asp Val Trp Gly Arg  
         110                    115                    120                    125

ggc acc atg gtc act gtc tcc tca ggt gga ggc ggt agc tcc tat gtg 433  
 Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Ser Tyr Val  
 5  
 130 135 140  
 ctg act cag cca ccc tcg gtg tca ggg tct cct gga cag tcg atc acc 481  
 10  
 Leu Thr Gln Pro Pro Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr  
 145 150 155  
 atc tcc tgc act gga acc agc agt gac gtt ggt ggt tat aac tat gtc 529  
 15  
 Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val  
 160 165 170  
 tec tgg tac caa cag cac cca ggc aaa gcc ccc aaa ctc atg att tat 577  
 20  
 Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr  
 175 180 185  
 gag ggc agt aaa cgg ccc tca ggg gtt tct aat cgc ttc tct ggc tcc 625  
 25  
 Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser  
 190 195 200 205  
 aag tct ggc aac acg gcc tcc ctg acc atc tct ggg ctc cag gct gag 673  
 30  
 Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu  
 210 215 220  
 gac gag gct gat tat tac tgc agc tca tat aca acc aga agc act cgg 721  
 35  
 Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Thr Arg Ser Thr Arg  
 225 230 235  
 gtg ttc ggc gga ggg acc aag ctg acc gtc cta gac tac aag gat gac 769  
 40  
 Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Asp Tyr Lys Asp Asp  
 240 245 250  
 gac gat aag tgataagcgg ccgc 792  
 50  
 Asp Asp Lys  
 255  
 55

<210> 111

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> sc4.3, PCR primer

<400> 111

ggtggctgag tcagcacata ggacgatccg ccaccaccog aaccaccacc acccgaacca 60  
cc 62

<210> 112

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> scl.3, PCR primer

<400> 112

gcaccatggt cactgtctcc tcaggtgggtg gtggttcggg tgggtggtggt tcgggtggtg 60  
g 61

<210> 113

<211> 822

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (11)... (807)

<223> scl2E10, Single chain Fv

&lt;400&gt; 113

5 gaattccacc atg aaa cat ctg tgg ttc ttc ctt ctc ctg gtg gca gct 49  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala  
 1 5 10  
 10 ccc aga tgg gtc ctg tcc cag gtg cag ctg cag cag tcg ggc cca gga 97  
 Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Gly  
 15 20 25  
 15 ctg gtg aag cct tcg gag acc ctg tcc ctc acc tgc act gtc tct ggt 145  
 Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
 20 30 35 40 45  
 gac tcc atc agt agt tac tac tgg agc tgg att cgg cag ccc cca ggg 193  
 Asp Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly  
 25 50 55 60  
 aag gga ctg gag tgg att ggg tat atc tat tac agt ggg agc acc aac 241  
 Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn  
 30 65 70 75  
 tac aac ccc tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc 289  
 Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser  
 35 80 85 90  
 aag agc cag ttc tcc ctg aag ctg agc tct gtg acc gcc gca gac acg 337  
 Lys Ser Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
 40 95 100 105  
 45 gcc gtg tat tac tgt gcg aga ggg cgg tac ttc gat gtc tgg ggc cgt 385  
 Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Phe Asp Val Trp Gly Arg  
 50 110 115 120 125  
 ggc acc atg gtc act gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt 433  
 Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 55 130 135 140

ggt tgc ggt ggt ggc gga tgc tcc tat gtg ctg act cag cca ccc tgc 481  
 5 Gly Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Pro Pro Ser  
                     145                    150                    155  
 gtg tca ggg tct cct gga cag tgc atc acc atc tcc tgc act gga acc 529  
 10 Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr  
                     160                    165                    170  
 agc agt gac gtt ggt ggt tat aac tat gtc tcc tgg tac caa cag cac 577  
 15 Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His  
                     175                    180                    185  
 cca ggc aaa gcc ccc aaa ctc atg att tat gag ggc agt aaa cgg ccc 625  
 20 Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Glu Gly Ser Lys Arg Pro  
                     190                    195                    200                    205  
 tca ggg gtt tct aat cgc ttc tct ggc tcc aag tct ggc aac acg gcc 673  
 25 Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala  
                     210                    215                    220  
 tcc ctg acc atc tct ggg ctc cag gct gag gac gag gct gat tat tac 721  
 30 Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr  
                     225                    230                    235  
 tgc agc tca tat aca acc aga agc act cgg gtg ttc ggc gga ggg acc 769  
 35 Cys Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr  
                     240                    245                    250  
 aag ctg acc gtc cta gac tac aag gat gac gac gat aag tgataagcgg 818  
 40 Lys Leu Thr Val Leu Asp Tyr Lys Asp Asp Asp Asp Lys  
                     255                    260                    265  
 50 ccgc 822

# 55 Claims

1. A modified antibody comprising two or more H chain V regions and two or more L chain V regions of antibody and showing TPO agonist action by crosslinking TPO receptor.

2. The modified antibody of claim 1, wherein the H chain V region and the L chain V region are connected through a linker.
3. The modified antibody of claim 2 or 3, wherein the linker is a peptide linker comprising at least one amino acid.
4. The modified antibody of any one of claims 1 to 3, wherein the modified monoclonal antibody is a multimer of single chain Fv comprising an H chain V region and an L chain V region.
5. The modified antibody of claim 4, wherein the modified antibody is composed of tetramer, trimer or dimer of single chain Fv.
6. The modified antibody of claim 5, wherein the modified antibody is composed of dimer of single chain Fv.
7. The modified antibody of any one of claims 4 to 6, wherein the H chain V region and the L chain V region existing in the same chain are not associated to form an antigen-binding site.
8. The modified antibody of any one of claims 1 to 3, wherein the modified antibody is a single chain polypeptide comprising two or more H chain V regions and two or more L chain V regions.
9. The modified antibody of claim 8, wherein the modified antibody is a single chain polypeptide comprising two H chain V regions and two L chain V regions.
10. The modified antibody of any one of claims 1 to 9, wherein the modified antibody further comprises an amino acid sequence(s) for peptide purification.
11. The modified antibody of any one of claims 1 to 10, wherein the modified antibody has been purified.
12. The modified antibody of any one of claims 1 to 11, wherein H chain V region and/or L chain V region is H chain V region and/or L chain V region derived from a human antibody.
13. The modified antibody of any one of claims 1 to 11, wherein H chain V region and/or L chain V region is humanized H chain V region and/or L chain V region.
14. The modified antibody of any one of claims 1 to 13, wherein the modified antibody is mono-specific modified antibody.
15. The modified antibody of any one of claims 1 to 13, wherein the modified antibody is multi-specific modified antibody.
16. The modified antibody of claim 15, wherein the modified antibody is bi-specific modified antibody.
17. The monoclonal antibody of claim 14, wherein the L chain V region and the H chain V region are from the same monoclonal antibody.
18. The monoclonal antibody of any one of claims 1 to 17 which shows an equivalent or better agonist action (ED50) compared with the parent monoclonal antibody.
19. The monoclonal antibody of claim 18 which shows at least 2-fold agonist action (ED50) compared with the parent monoclonal antibody.
20. The monoclonal antibody of claim 19 which shows at least 10-fold agonist action (ED50) compared with the parent monoclonal antibody.
21. The monoclonal antibody of any one of claims 1 to 17 which is derived from a parent antibody having substantially no agonist action.
22. A compound comprising two or more H chain V regions and two or more L chain V regions of monoclonal antibody and showing an equivalent or better agonist action (ED50) compared with thrombopoietin (TPO).

23. The compound of claim 22 which shows at least 2-fold agonist action (ED50) compared with TPO.
24. The compound of claim 23 which shows at least 10-fold agonist action (ED50) compared with TPO.
- 5 25. The modified monoclonal antibody or compound of any one of claims 1-24 which has ED50 of TPO agonist activity not more than 20pM.
26. The modified monoclonal antibody or compound of claim 25 which has ED50 of TPO agonist activity not more than 10pM.
- 10 27. The modified monoclonal antibody or compound of claim 26 which has ED50 of TPO agonist activity not more than 2pM.
28. The modified antibody or compound of any one of claims 1 to 27 which has intercellular adhesion action (ED50) not more than 1/10 compared with the parent antibody.
- 15 29. The modified antibody or compound of any one of claims 1 to 27 which has substantially no intercellular adhesion action.
30. A DNA which encodes the modified antibody or compound of any one of claims 1 to 29.
31. An animal cell which produces the modified antibody or compound of any one of claims 1 to 29.
32. A microorganism which produces the modified antibody or compound of any one of claims 1 to 29.
- 25 33. Use of the modified antibody or compound of any one of claims 1 to 29 as TPO agonist.
34. A method of causing an agonist action to cells by crosslinking TPO receptor using the modified antibody or compound of any one of claims 1 to 29 thereby transducing a signal into cells.
- 30 35. The method of claim 34 wherein the agonist action is proliferation, differentiation-induction or growth stimulation of megakaryocytes, platelet production or phosphorylation of TPO receptor protein.
36. A medicine comprising as active ingredient the modified antibody or compound of any one of claims 1 to 29.
- 35 37. The medicine of claim 36 which is for the treatment of thrombocytopenia.
38. Use of the modified antibody or compound of any one of claims 1 to 29 as medicine.
- 40 39. A method of screening a modified antibody comprising two or more H chain V regions and two or more L chain V regions of antibody and showing an agonist action by crosslinking TPO receptor which comprises the steps
  - (1) to produce a modified antibody comprising two or more H chain V regions and two or more L chain V regions of antibody and binding specifically to TPO receptor,
  - 45 (2) to subject cells expressing said TPO receptor to react with the modified antibody and
  - (3) to measure TPO agonist action in the cells caused by crosslinking TPO receptor.
40. A method of measuring an agonist action of a modified antibody comprising two or more H chain V regions and two or more L chain V regions of antibody and showing an agonist action by crosslinking TPO receptor which comprises the steps
  - (1) to produce a modified antibody comprising two or more H chain V regions and two or more L chain V regions of antibody and binding specifically to TPO receptor,
  - 50 (2) to subject cells expressing said TPO receptor to react with the modified antibody and
  - 55 (3) to measure TPO agonist action in the cells caused by crosslinking TPO receptor.

Fig. 1

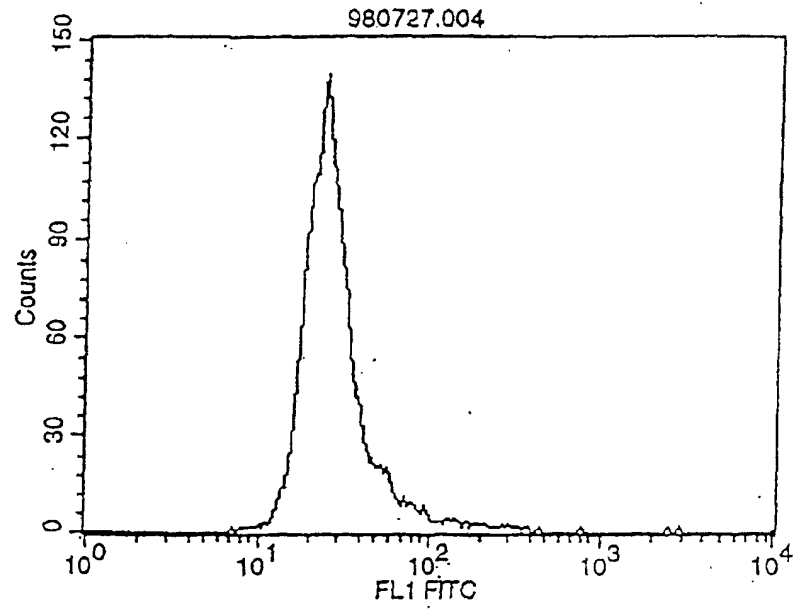


Fig. 2

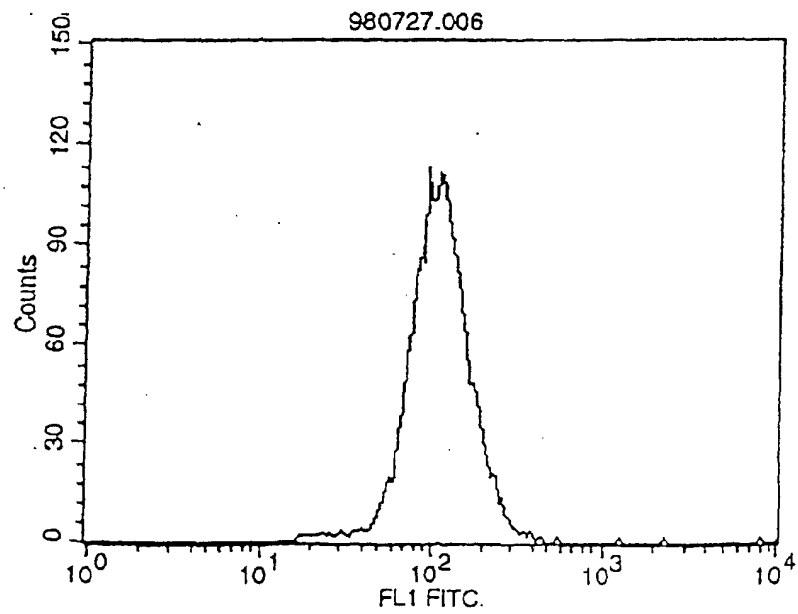


Fig. 3

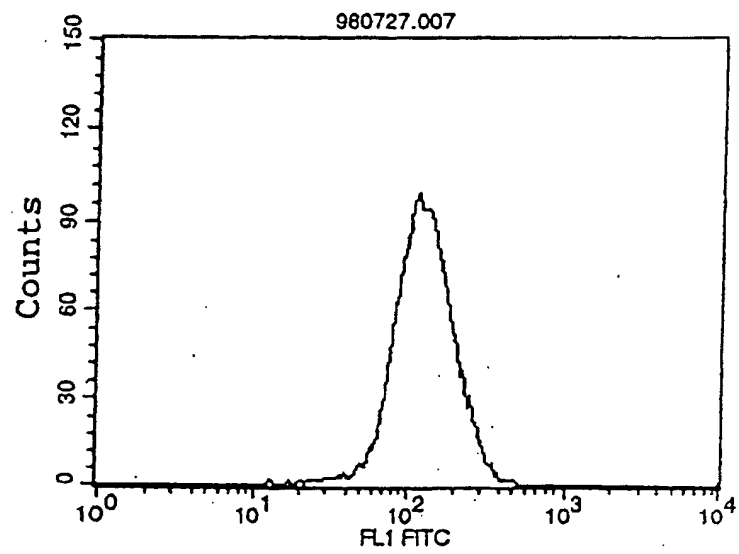


Fig. 4

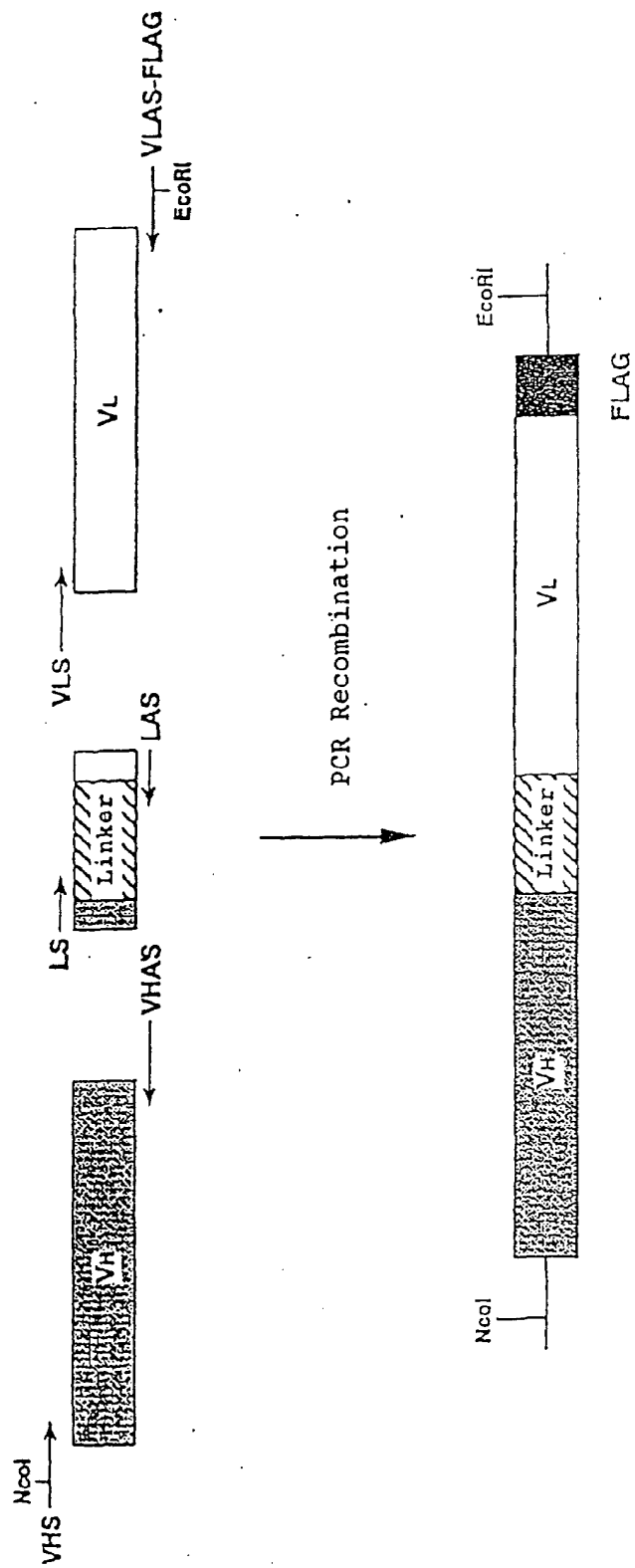


Fig. 5

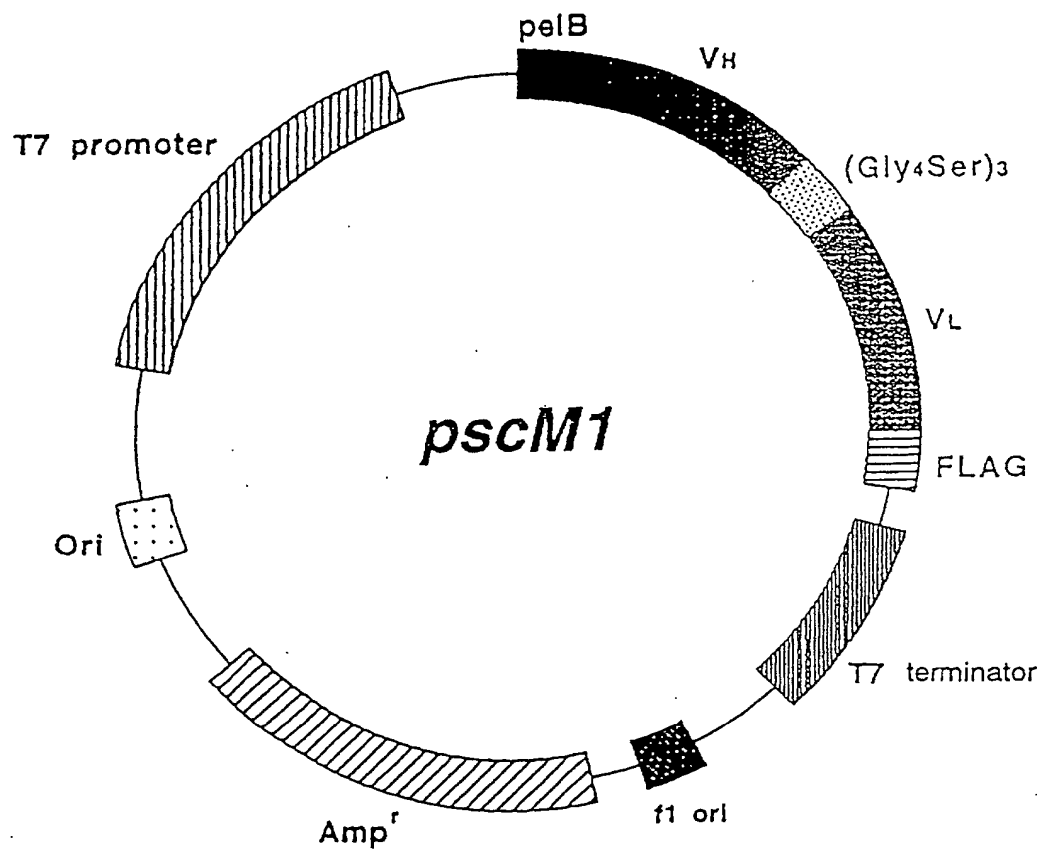


Fig. 6

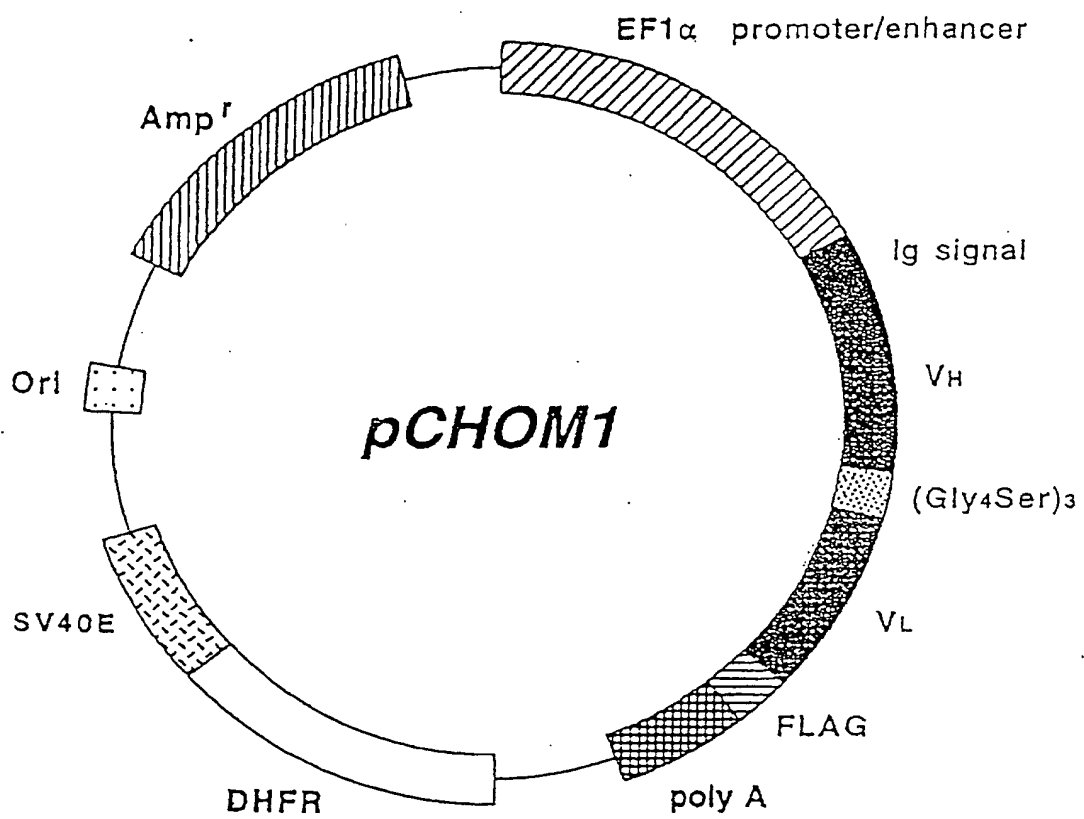


Fig. 7

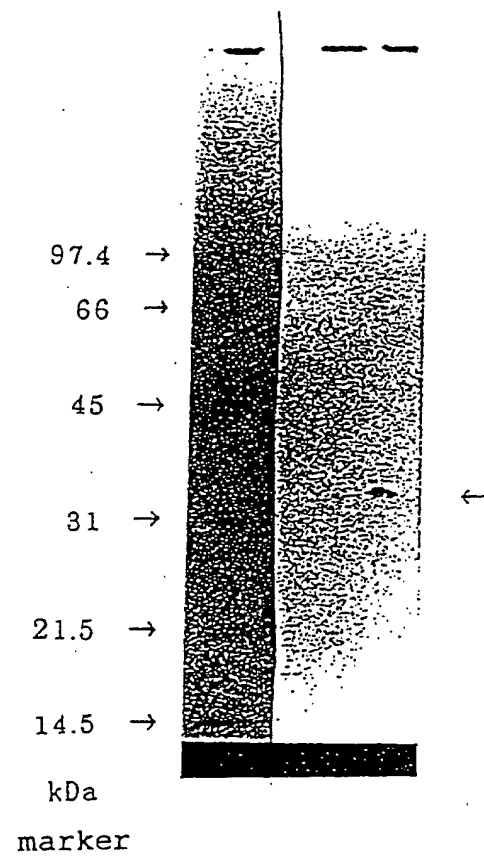


Fig. 8

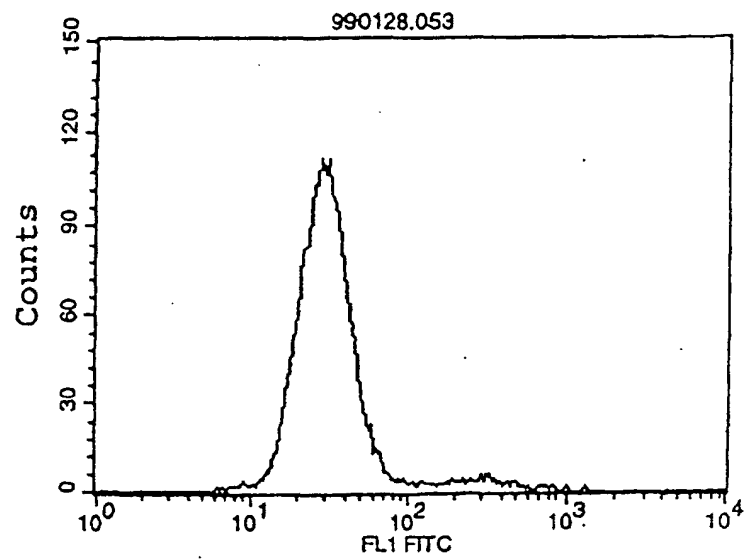


Fig. 9

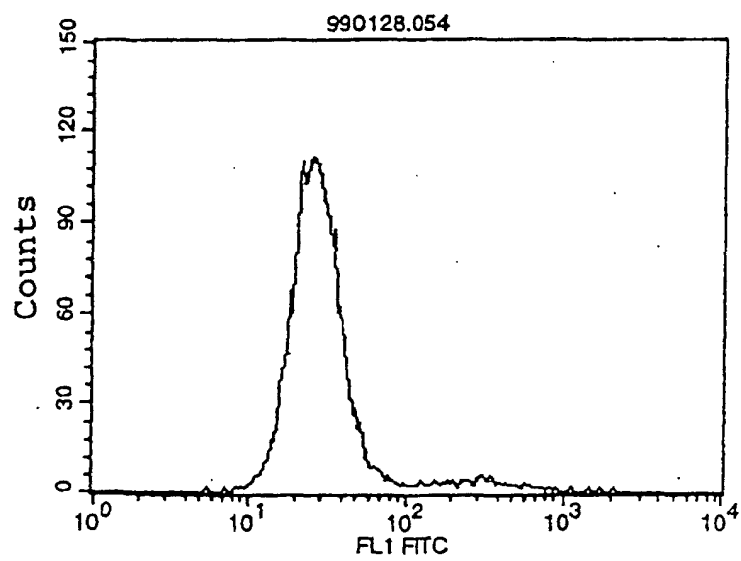


Fig. 10

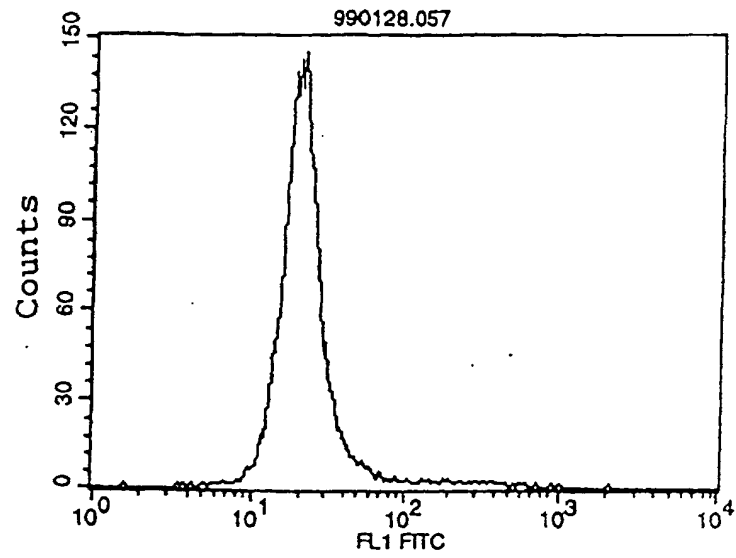


Fig. 11

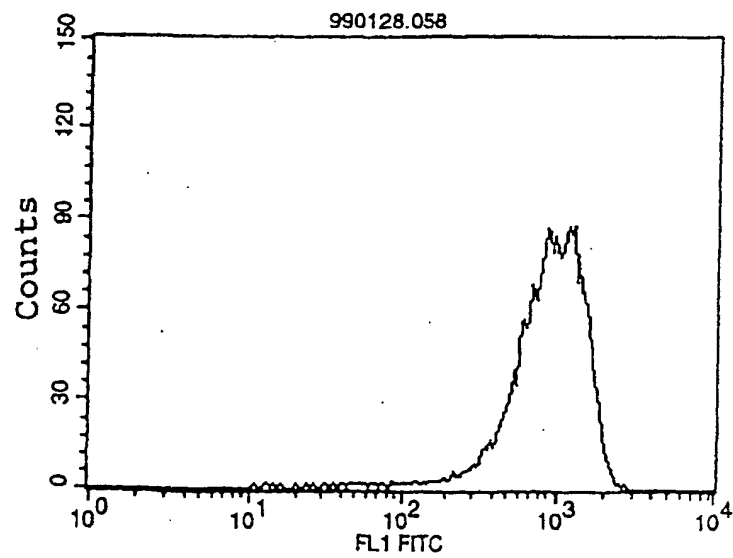


Fig. 12

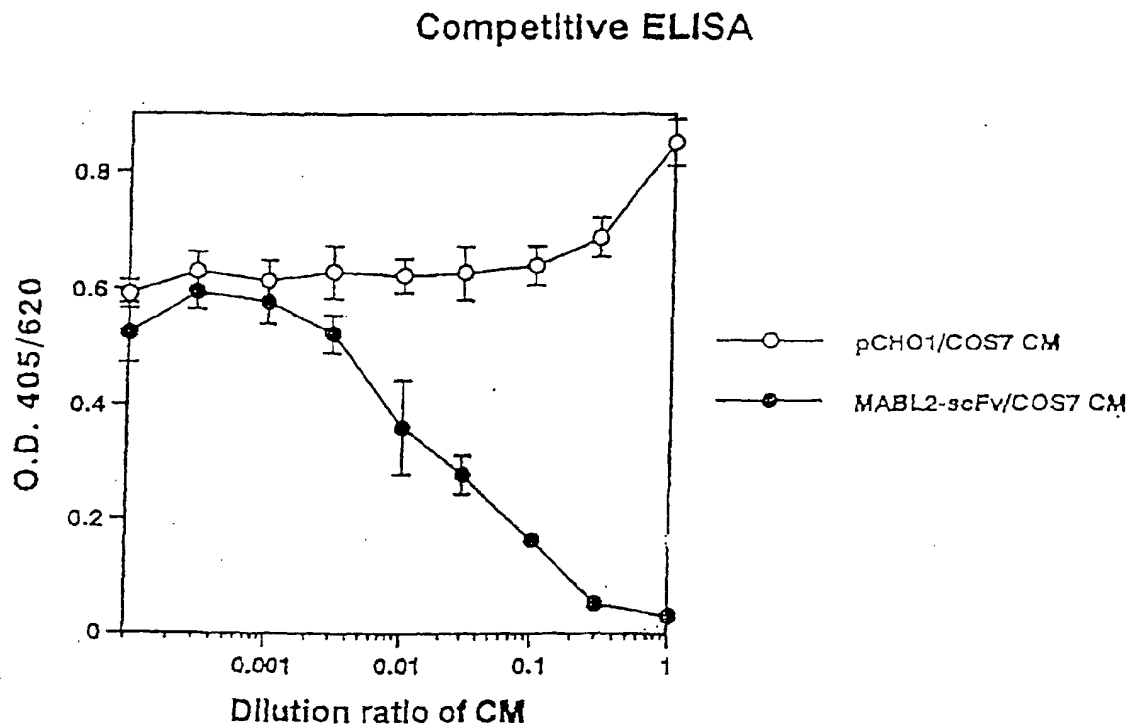


Fig. 13

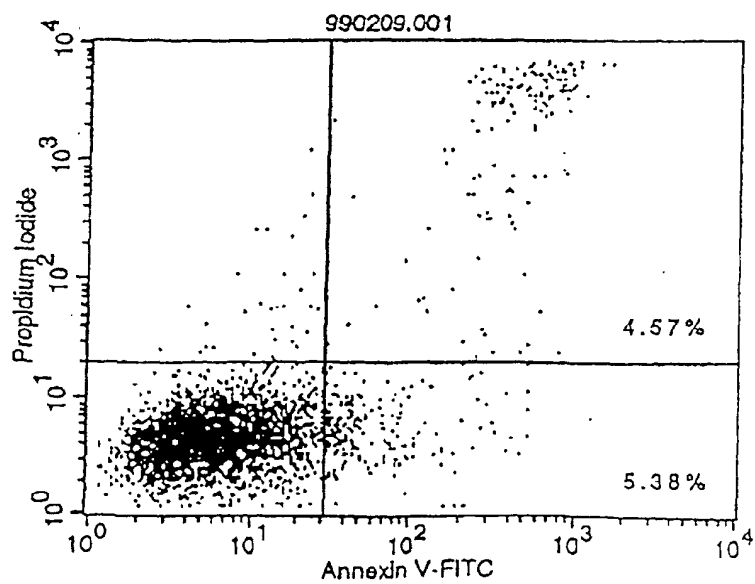


Fig. 14

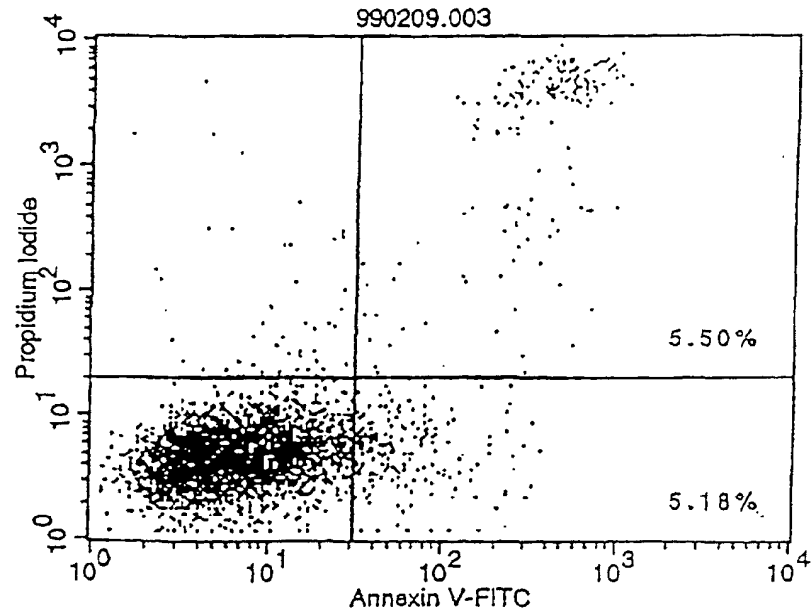


Fig. 15

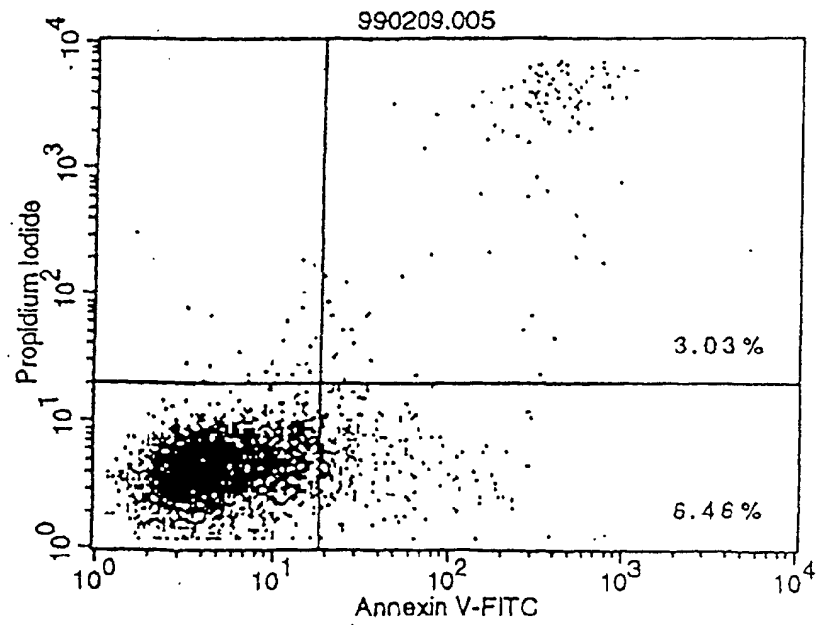


Fig. 16

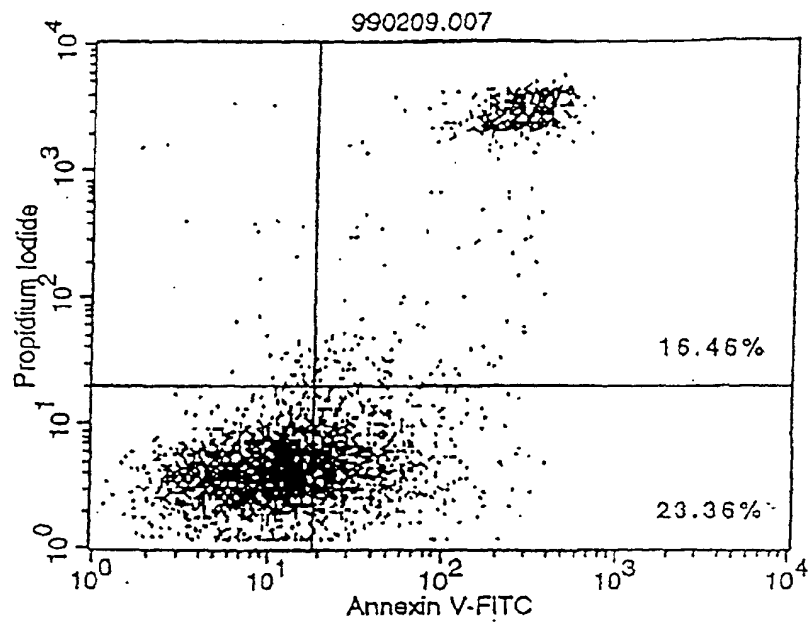


Fig. 17

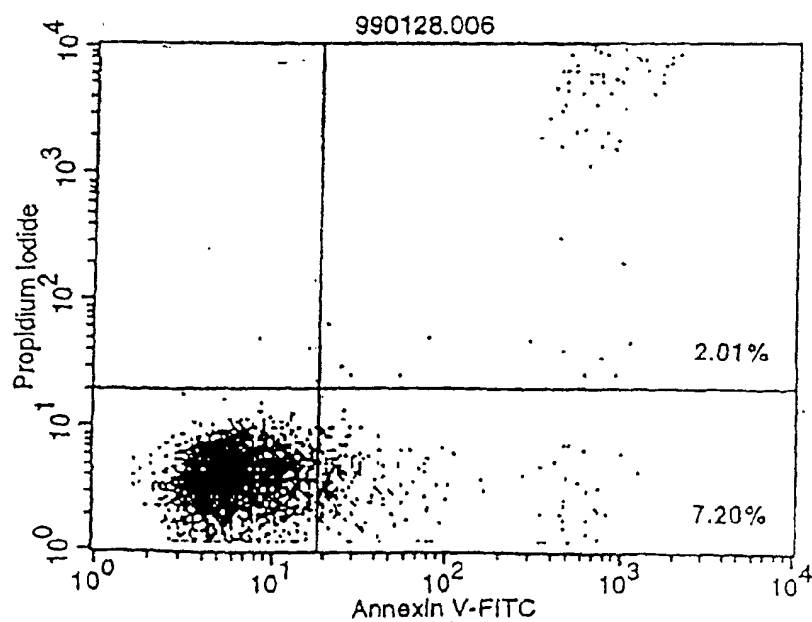


Fig. 18

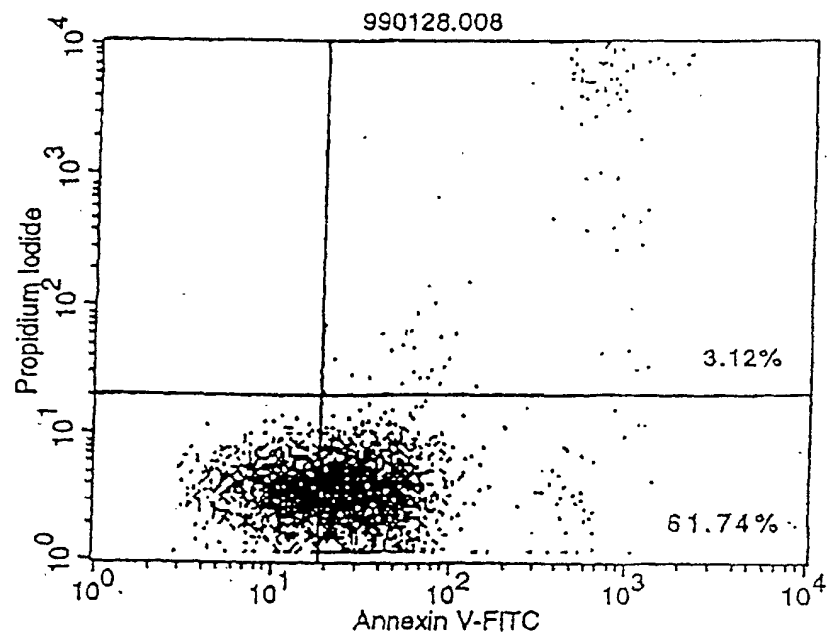


Fig. 19

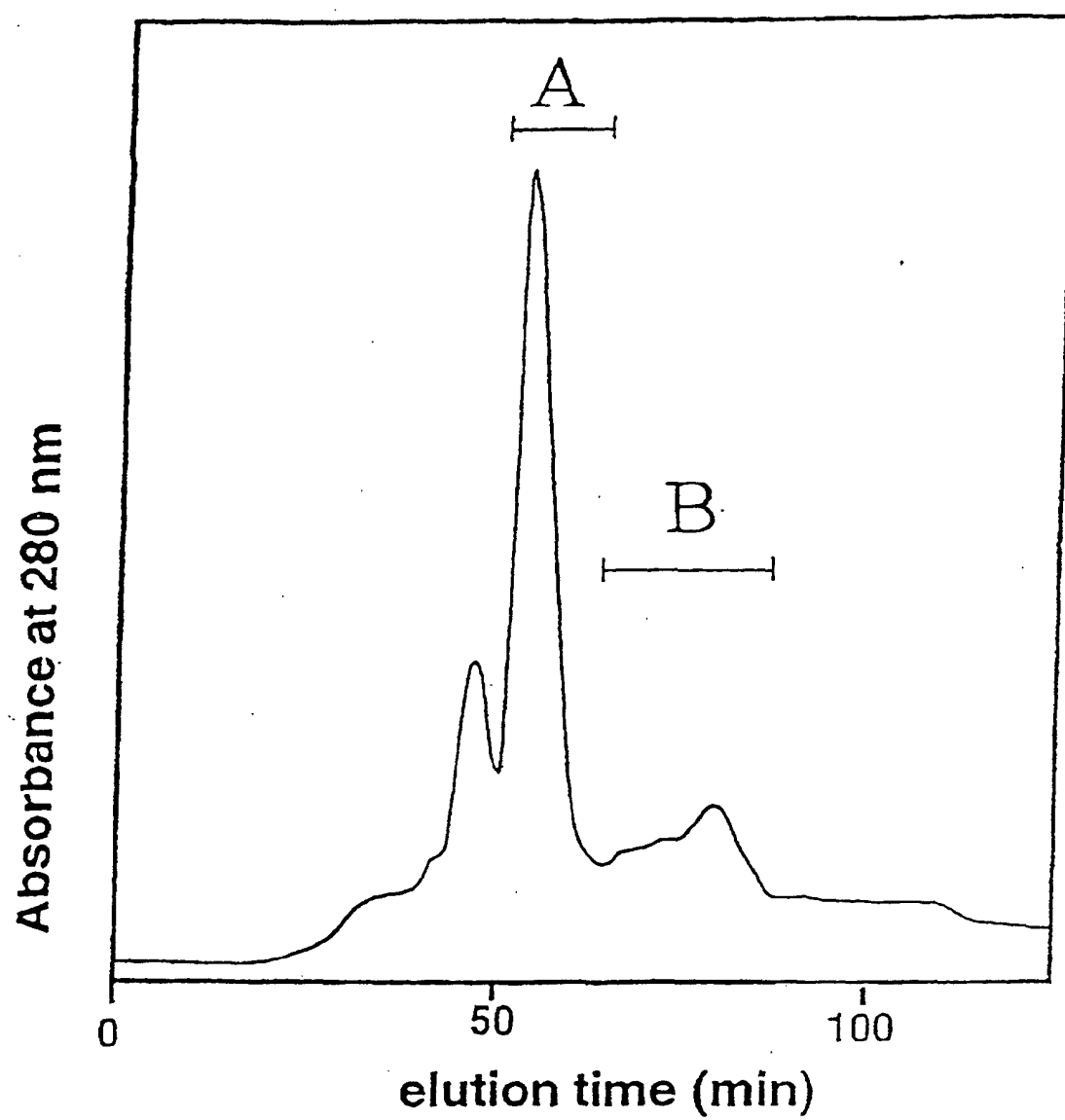


Fig. 20

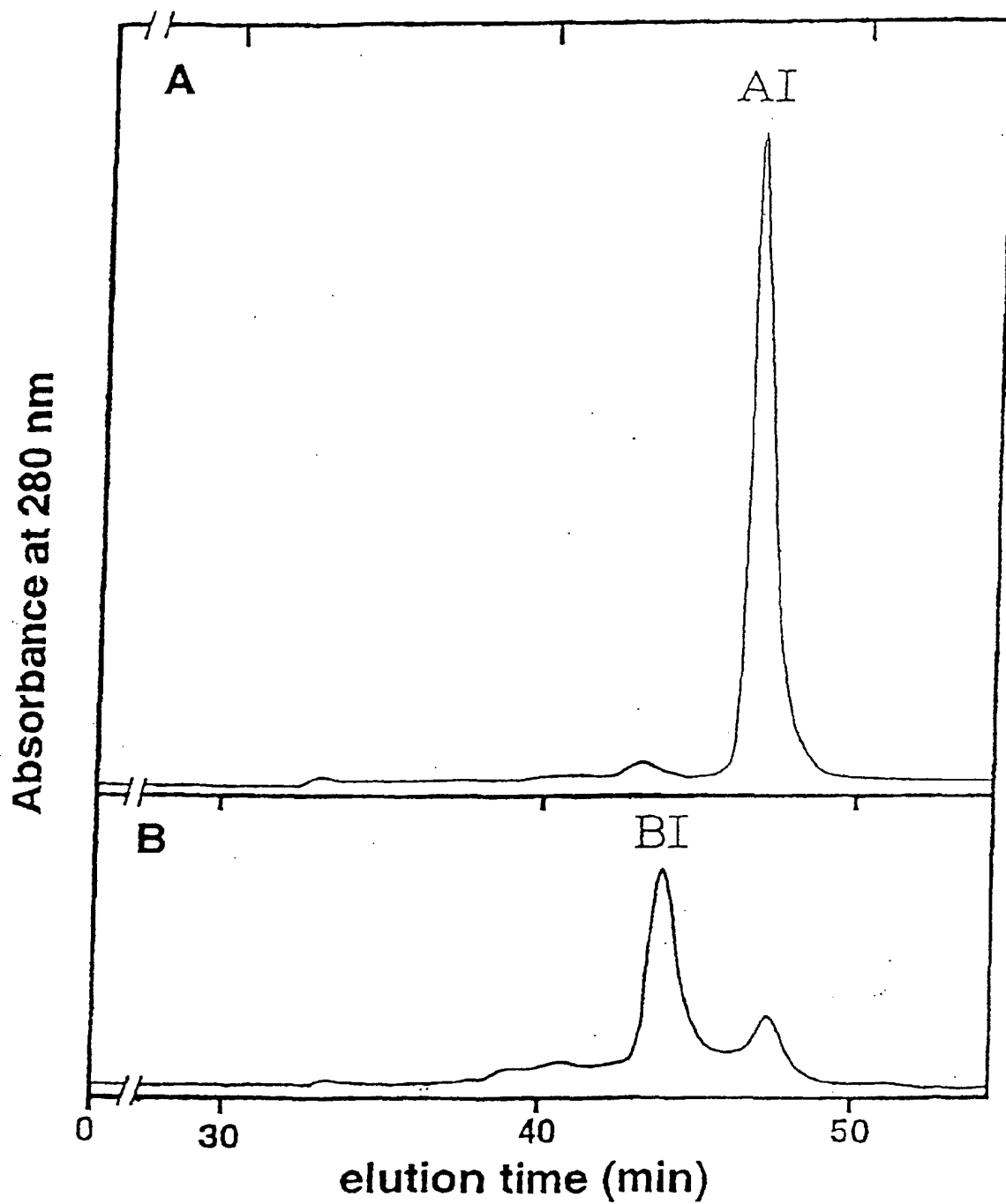


Fig. 21

## SDS-PAGE analysis of MABL2-scFv

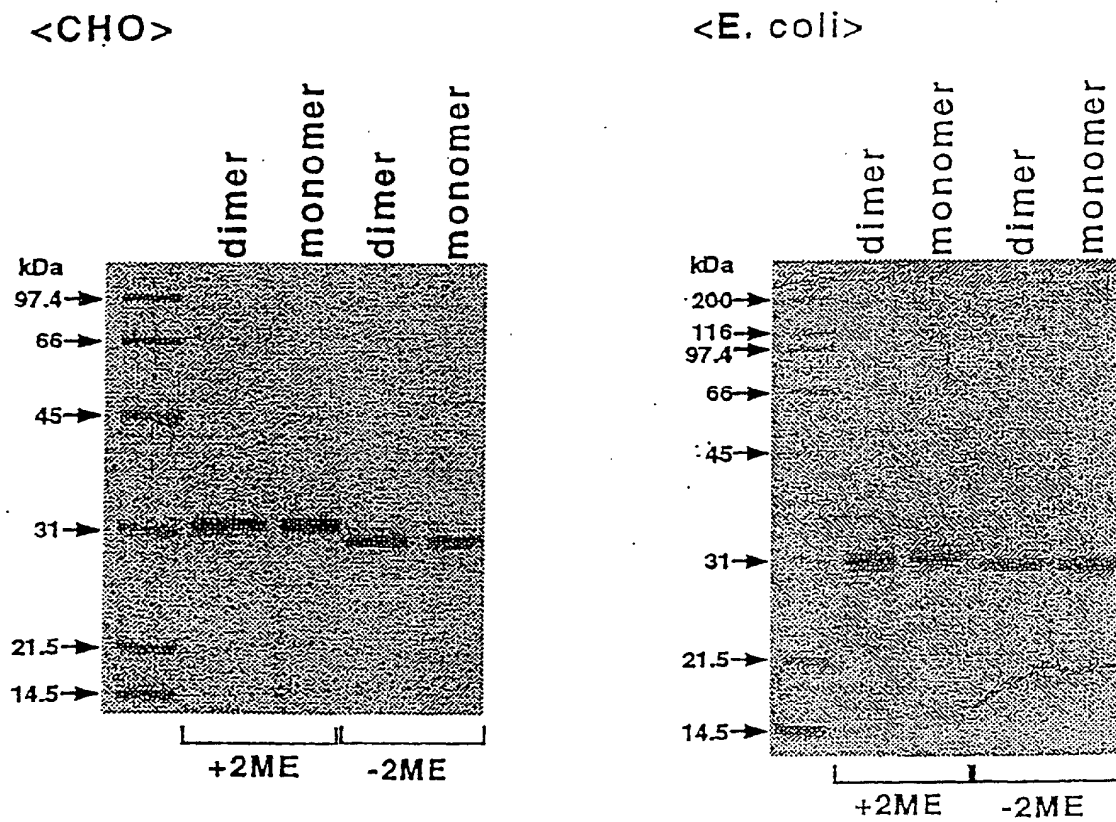


Fig. 22

TSK gel G3000SW

20 mM Acetate buffer, 0.15 M NaCl, pH 6.0

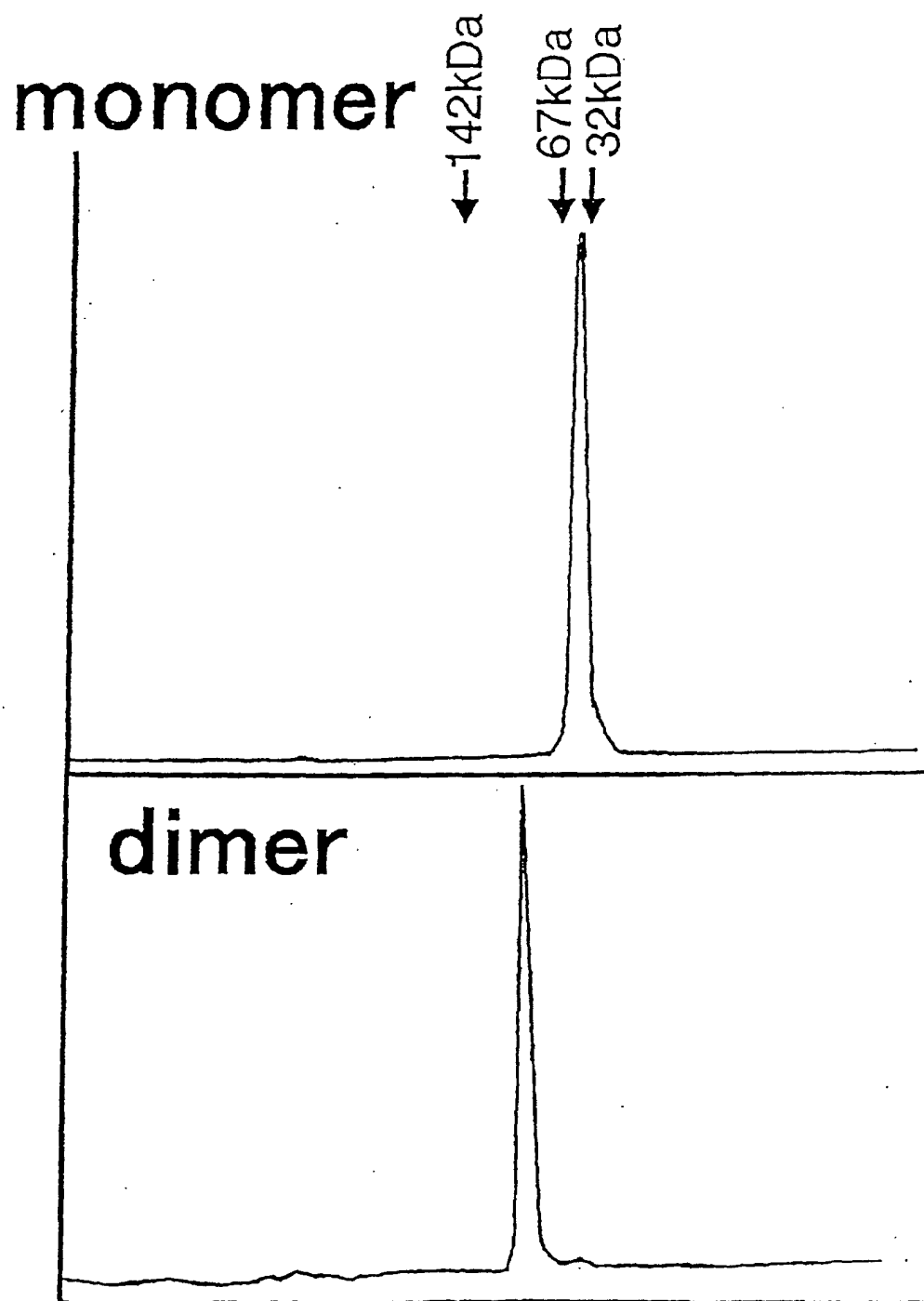


Fig. 23

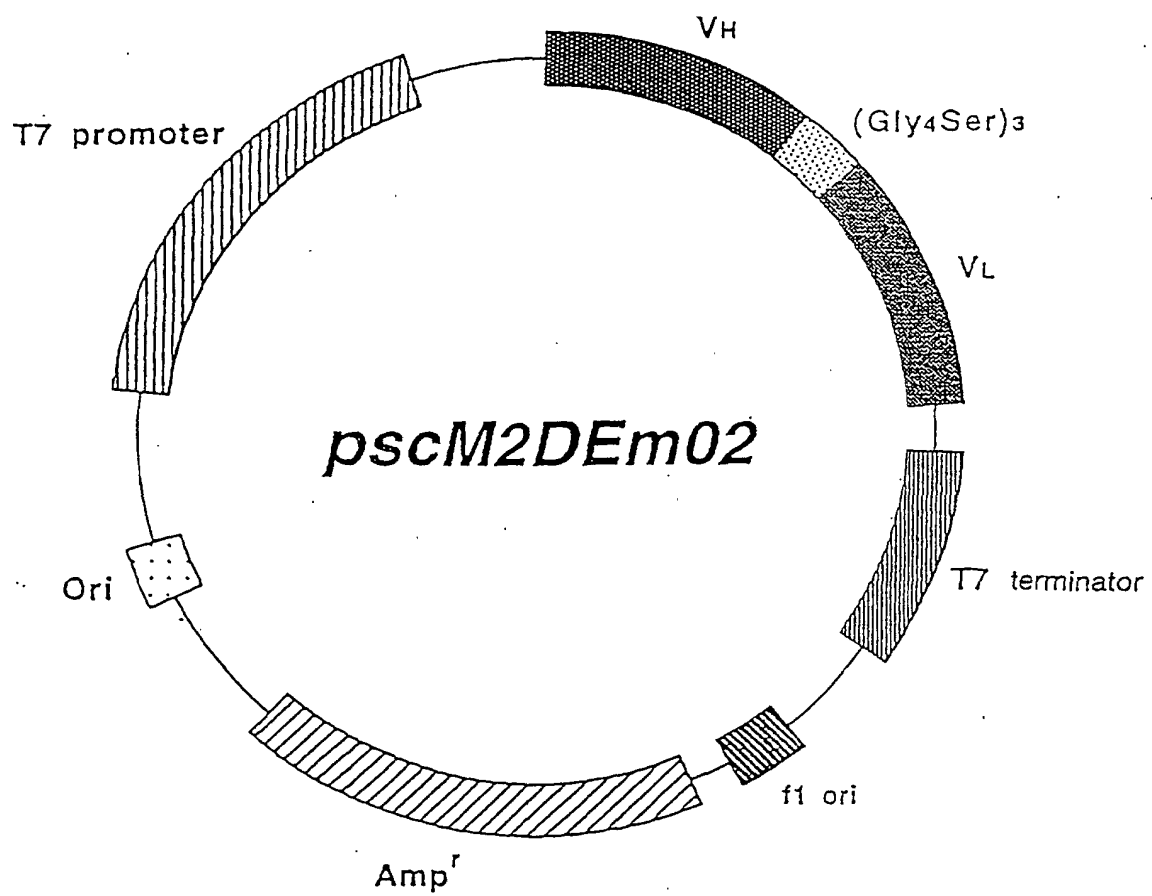


Fig. 24

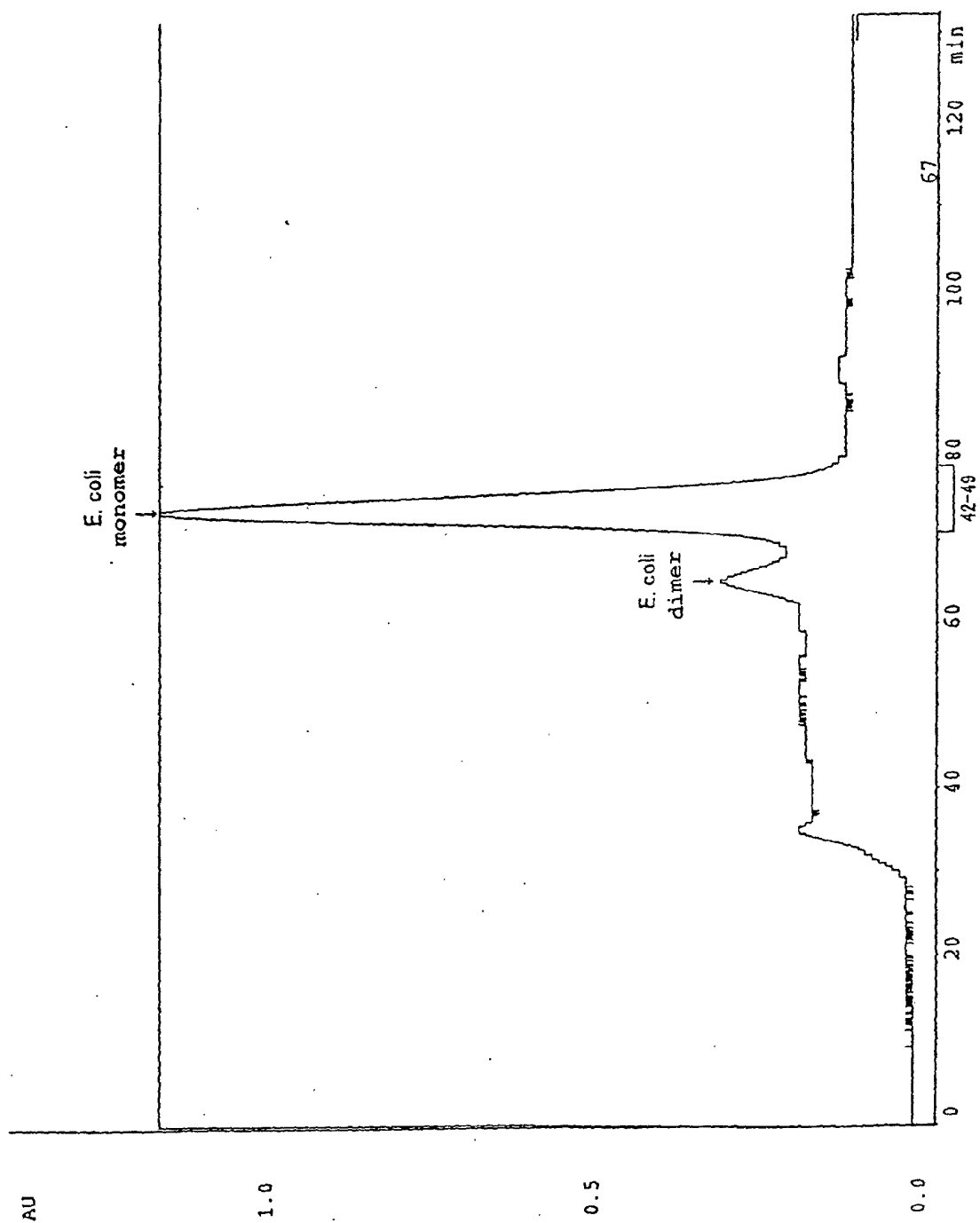


Fig. 25

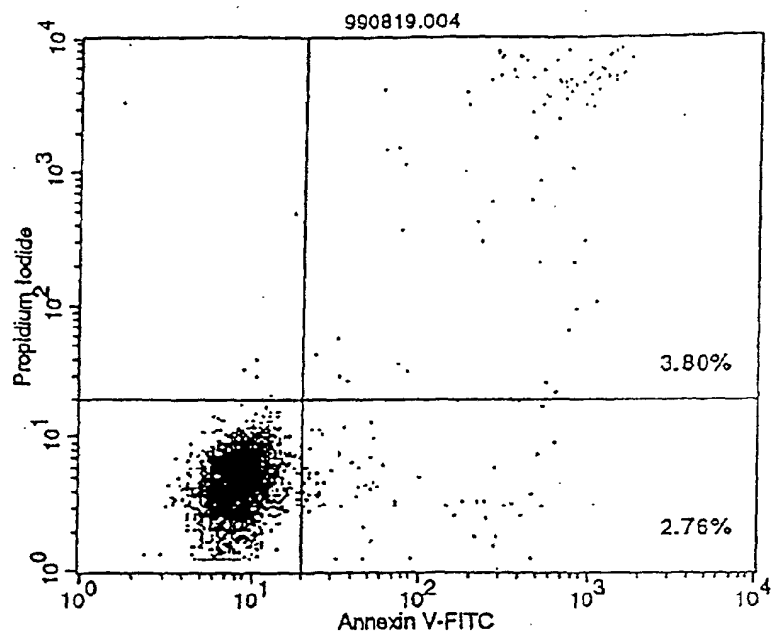


Fig. 26

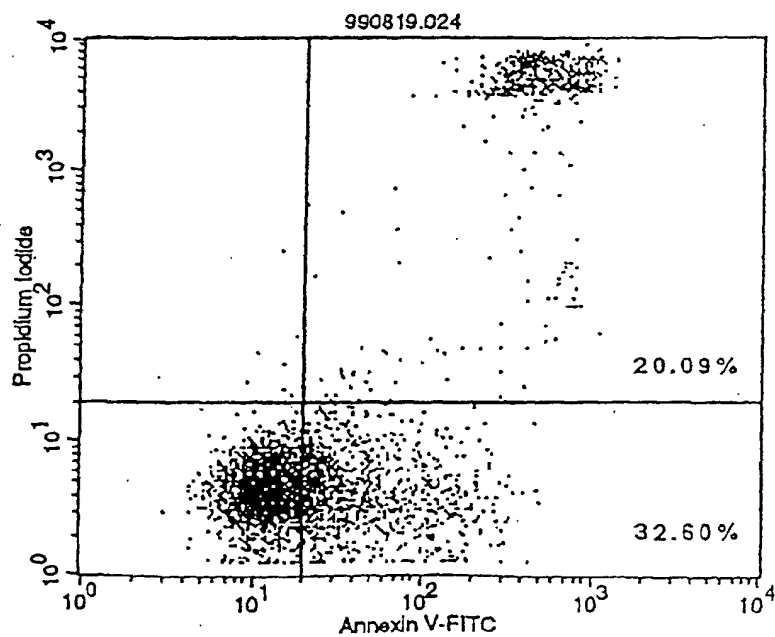


Fig. 27

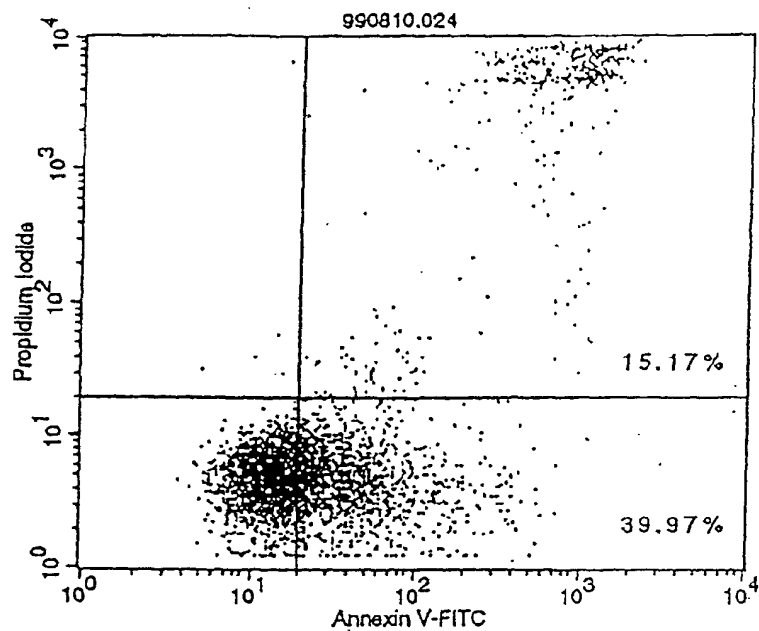


Fig. 28

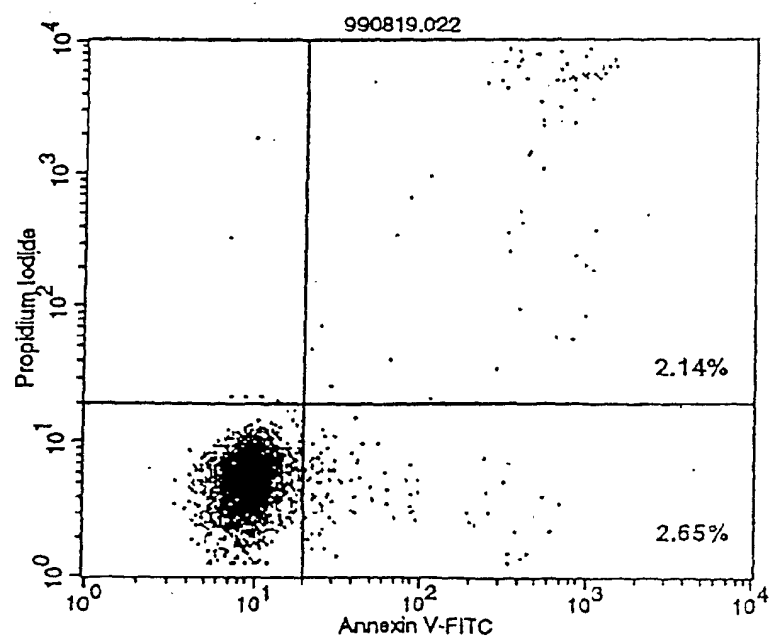


Fig. 29

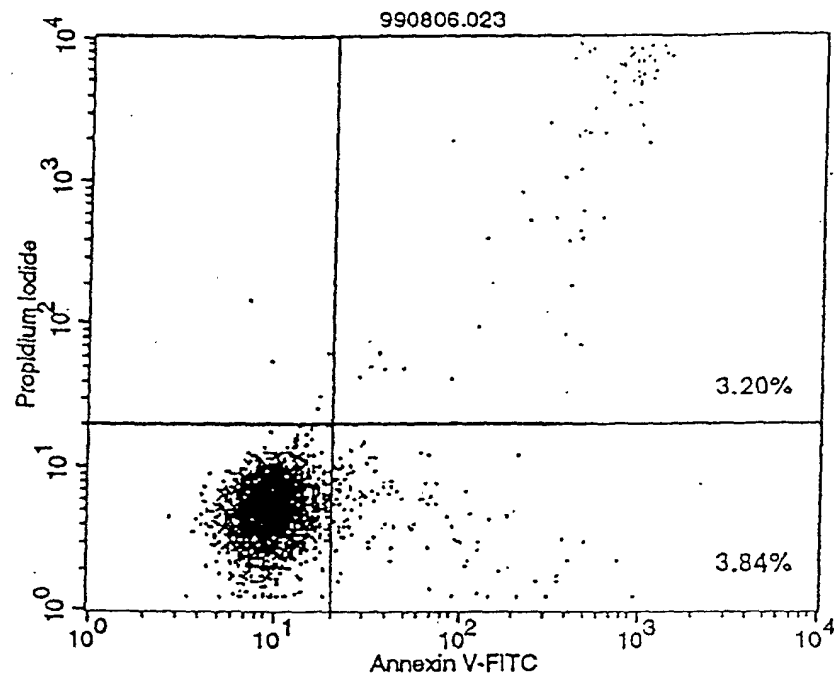


Fig. 30

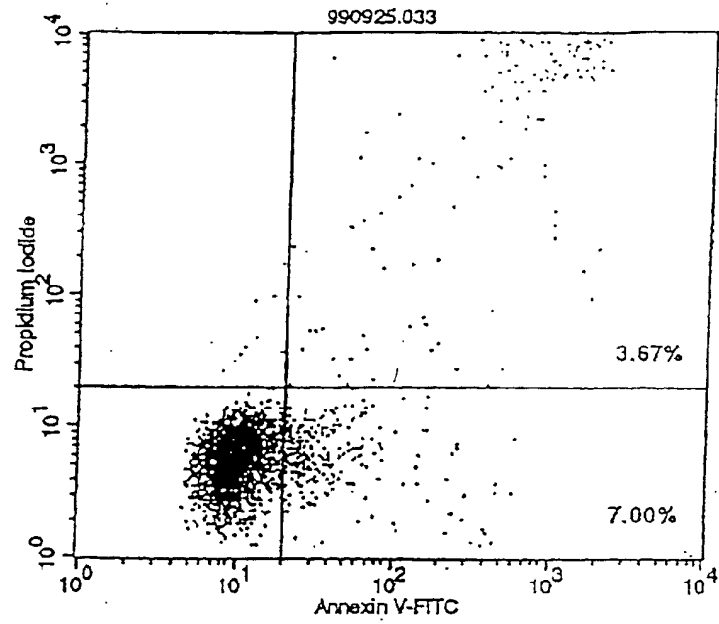


Fig. 31

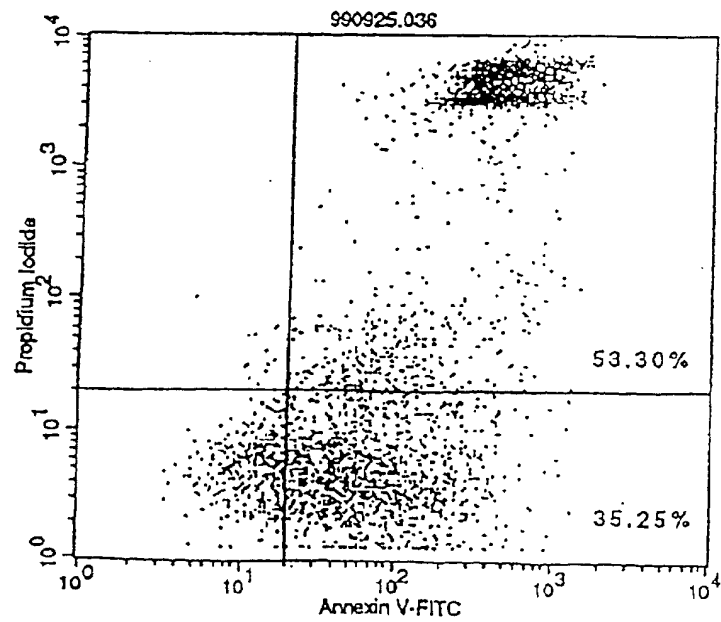
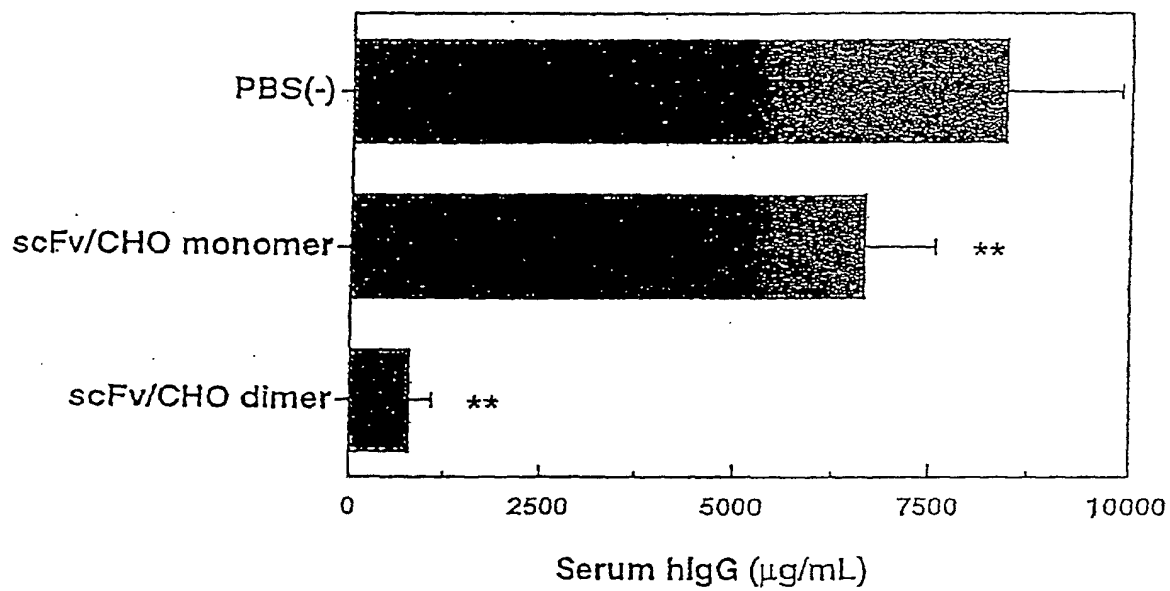


Fig. 32

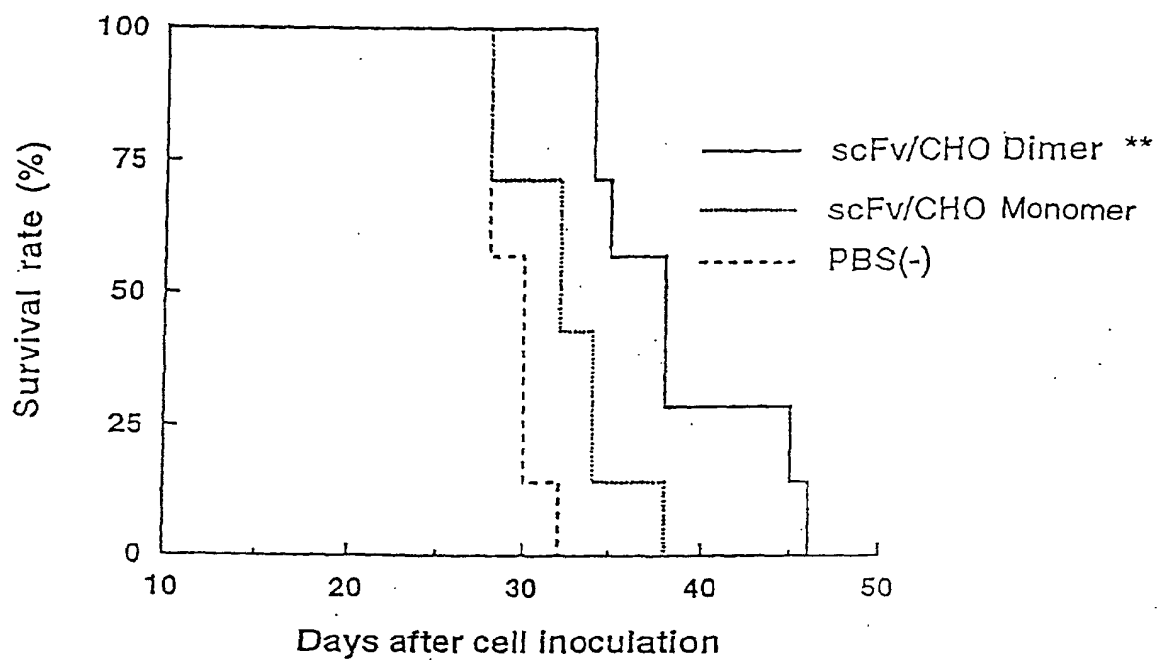
*Effect of MABL-2 (scFv) on serum hlgG  
in KPMM2 i.v. SCID mice*



\*\* :  $p < 0.01$

Fig. 33

*Effect of MABL-2 (scFv) on survival  
of KPMM2 i.v. SCID mice*



\*\* ;  $P < 0.01$  by t-test

Fig. 34

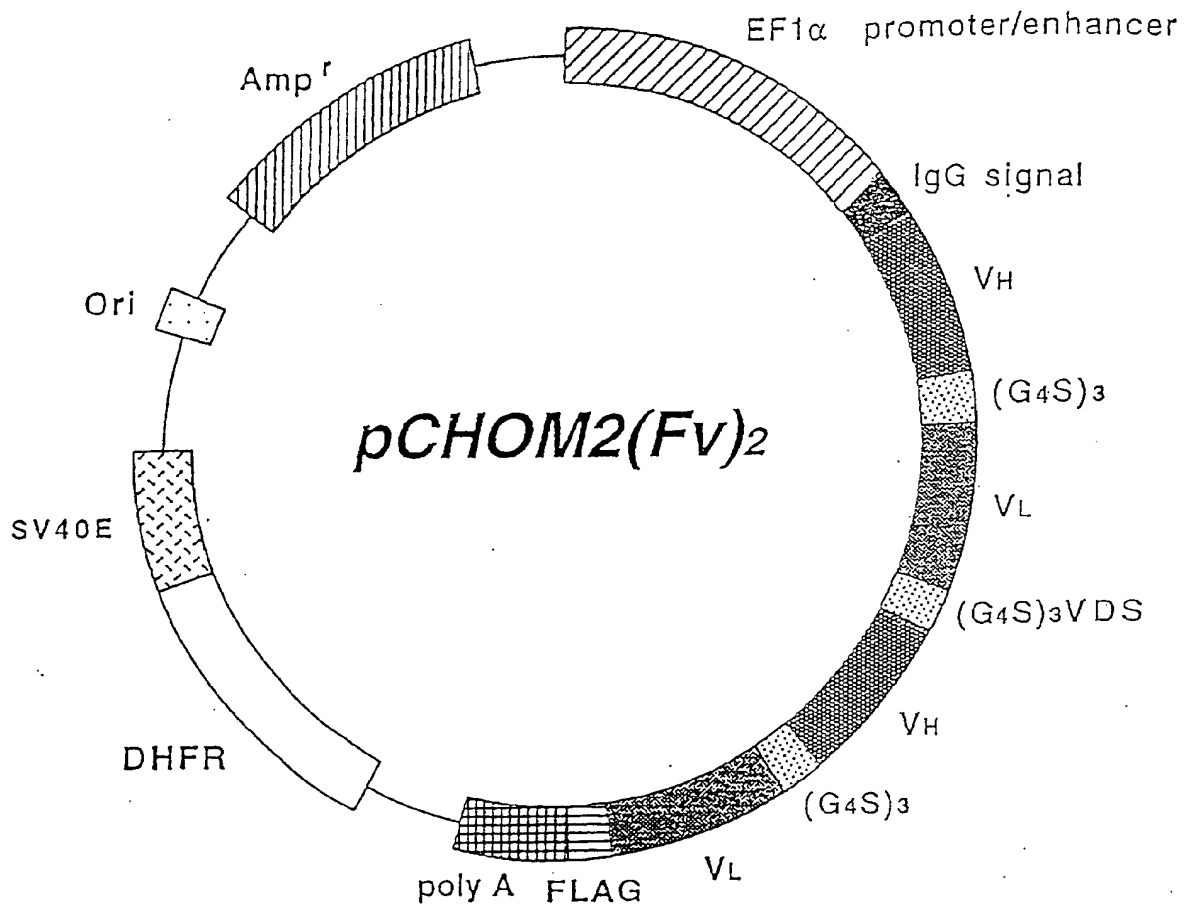


Fig. 35

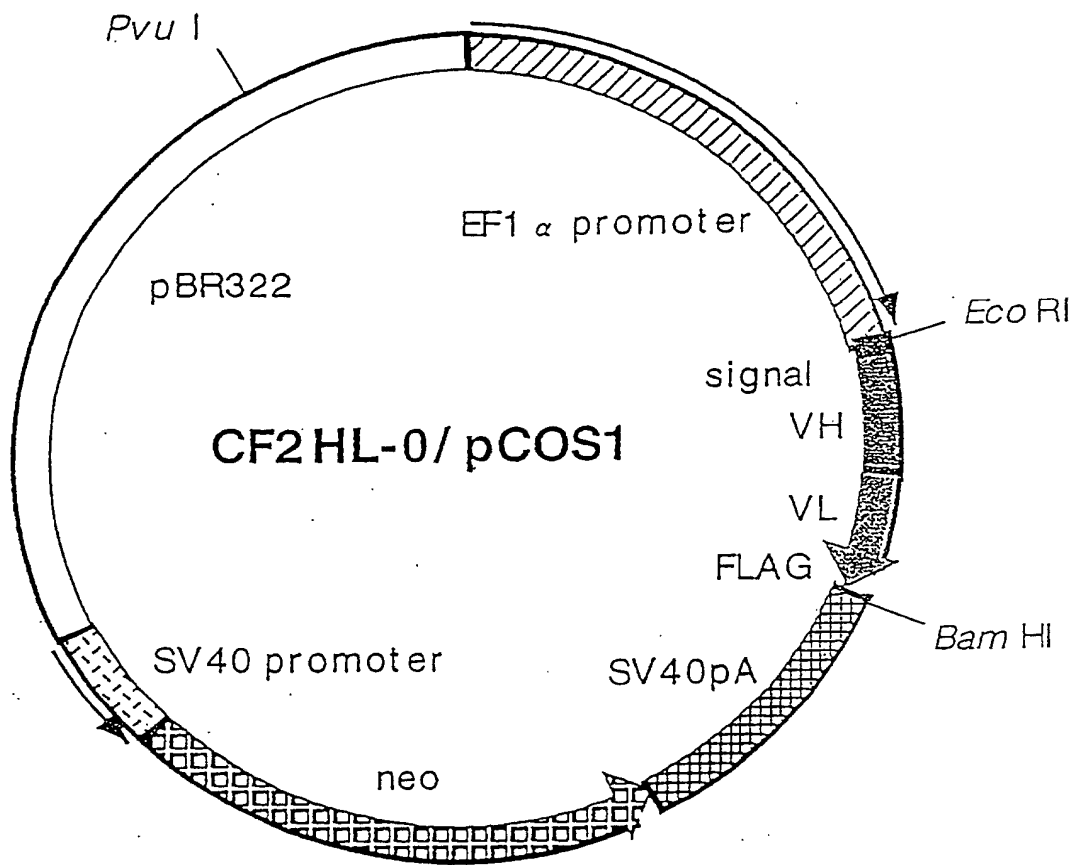
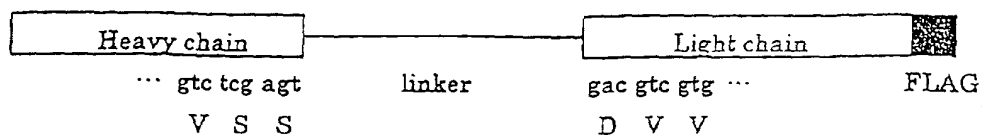


Fig. 36

Base Sequence and Amino Acid Sequence of Linker for HL Type



| Plasmid       | Number of<br>linker amino acid | linker   | linker               |
|---------------|--------------------------------|--|----------------------|
| CF2HL-0/pCOS1 | 0                              | gtc tcg agt<br>V S S                                       | gac gtc gtg<br>D V V |
| CF2HL-3/pCOS1 | 3                              | gtc tcg agt ggt ggt tcc<br>V S S G G S                     | gac gtc gtg<br>D V V |
| CF2HL-4/pCOS1 | 4                              | gtc tcg agt ggt ggt ggt tcc<br>V S S G G G S               | gac gtc gtg<br>D V V |
| CF2HL-5/pCOS1 | 5                              | gtc tcg agt ggt ggt ggt ggt tcc<br>V S S G G G G S         | gac gtc gtg<br>D V V |
| CF2HL-6/pCOS1 | 6                              | gtc tcg agt gt ggt ggt ggt ggt tcc<br>V S S G G G G G S    | gac gtc gtg<br>D V V |
| CF2HL-7/pCOS1 | 7                              | gtc tcg agt ggt ggt ggt ggt ggt tcc<br>V S S G G G G G G S | gac gtc gtg<br>D V V |

Fig. 37

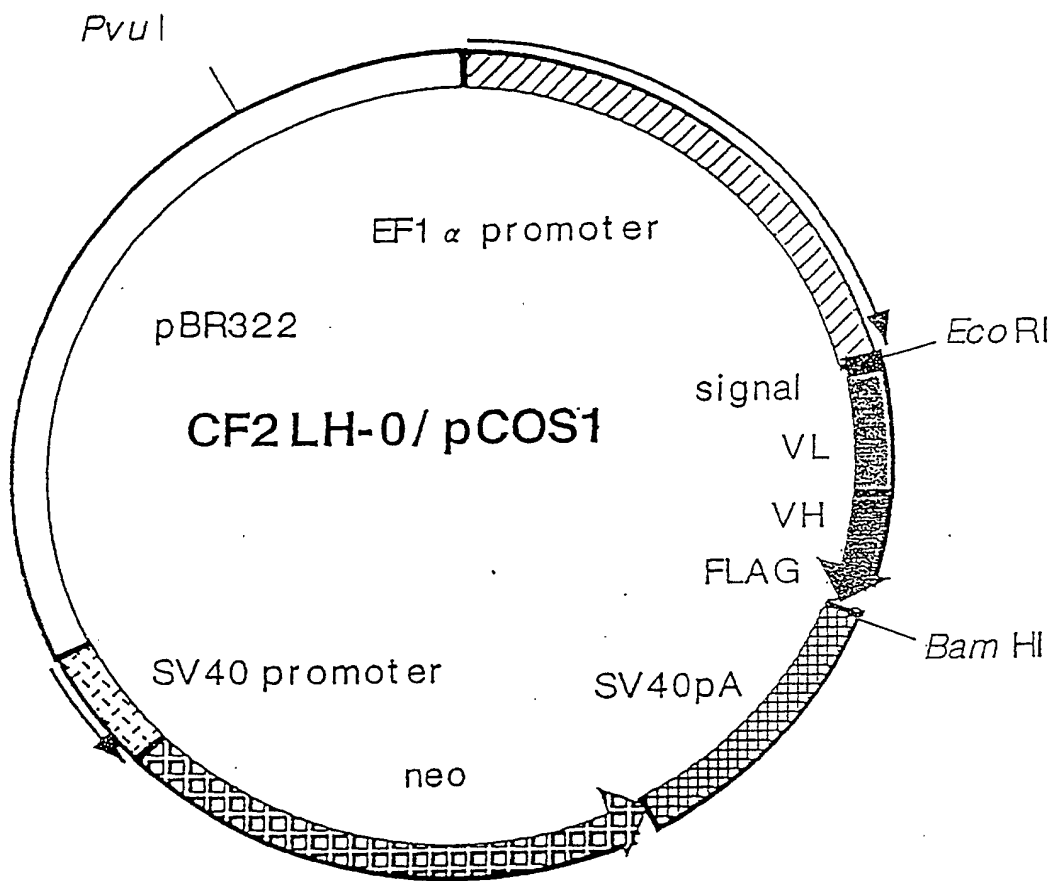


Fig. 38

Base Sequence and Amino Acid Sequence of Linker for LH Type

|                 |  |             |                 |
|-----------------|--|-------------|-----------------|
| Light chain     |  | Heavy chain |                 |
| ... gag ata aaa |  | linker      | cag gtc caa ... |
| E I K           |  |             | Q V Q           |
| FLAG            |  |             |                 |

| Plasmid       | Number of<br>linker amino acid | linker  |
|---------------|--------------------------------|---|
| CF2LH-0/pCOS1 | 0                              | <div>gag ata aaa</div> <div>E I K</div>   |
| CF2LH-3/pCOS1 | 3                              | <div>gag ata aaa tcc gga ggc</div> <div>E I K S G G</div>                         |
| CF2LH-4/pCOS1 | 4                              | <div>gag ata aaa tcc gga ggt ggc</div> <div>E I K S G G G</div>                   |
| CF2LH-5/pCOS1 | 5                              | <div>gag ata aaa tcc gga ggt ggt ggc</div> <div>E I K S G G G G</div>             |
| CF2LH-6/pCOS1 | 6                              | <div>gag ata aaa tcc gga ggt ggt ggt ggc</div> <div>E I K S G G G G G</div>       |
| CF2LH-7/pCOS1 | 7                              | <div>gag ata aaa tcc gga ggt ggt ggt ggt ggc</div> <div>E I K S G G G G G G</div> |

Fig. 39

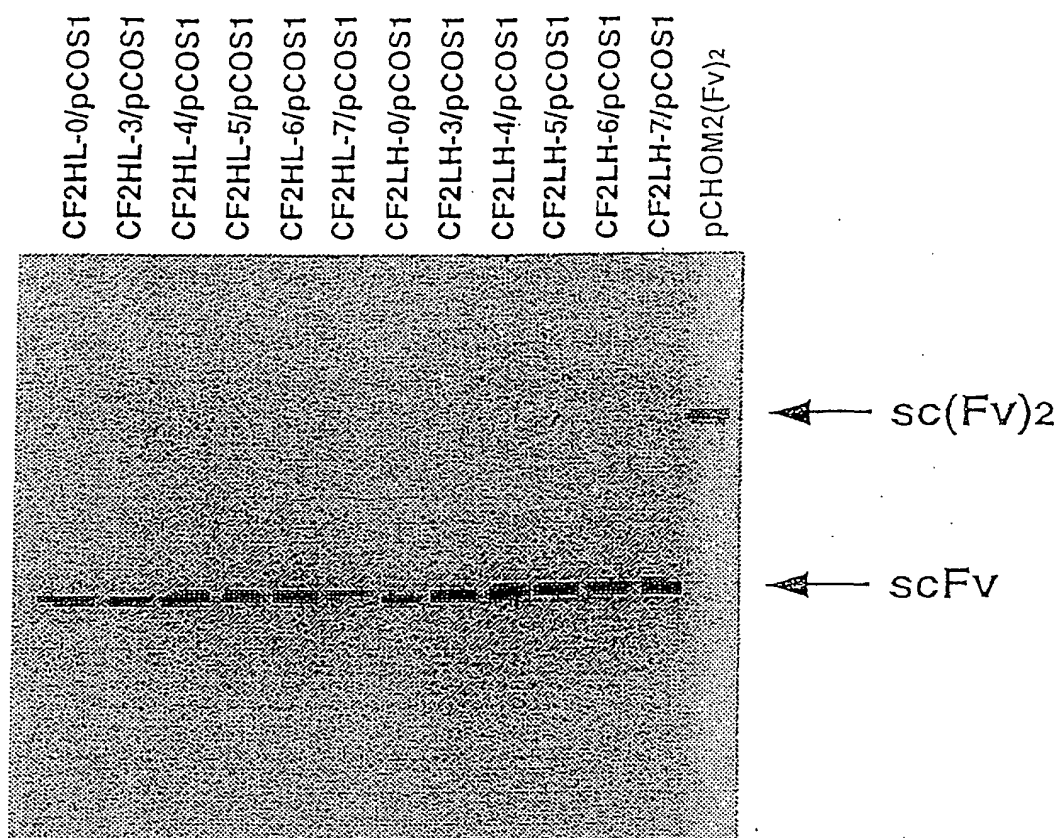


Fig. 40a

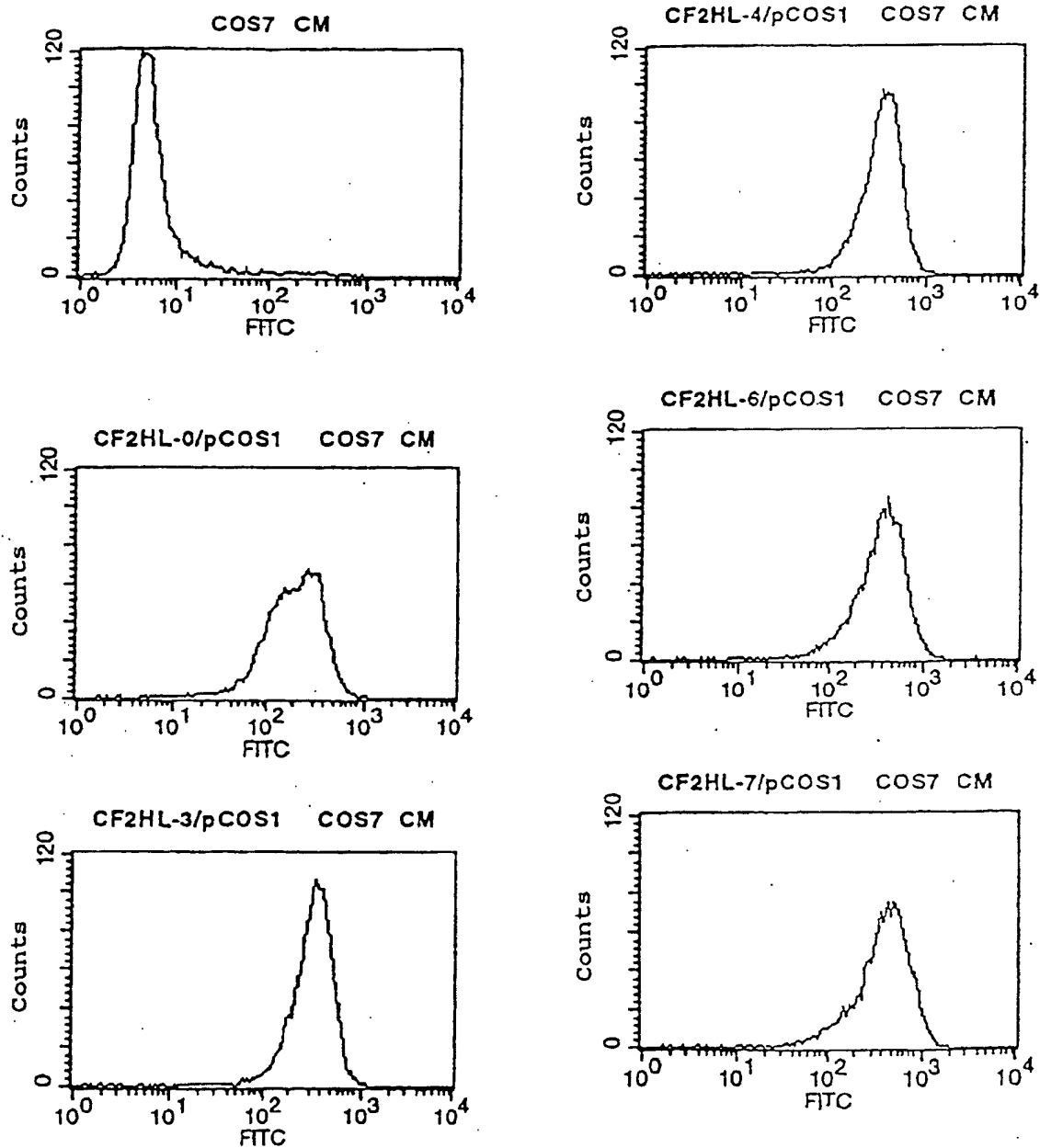


Fig. 40b

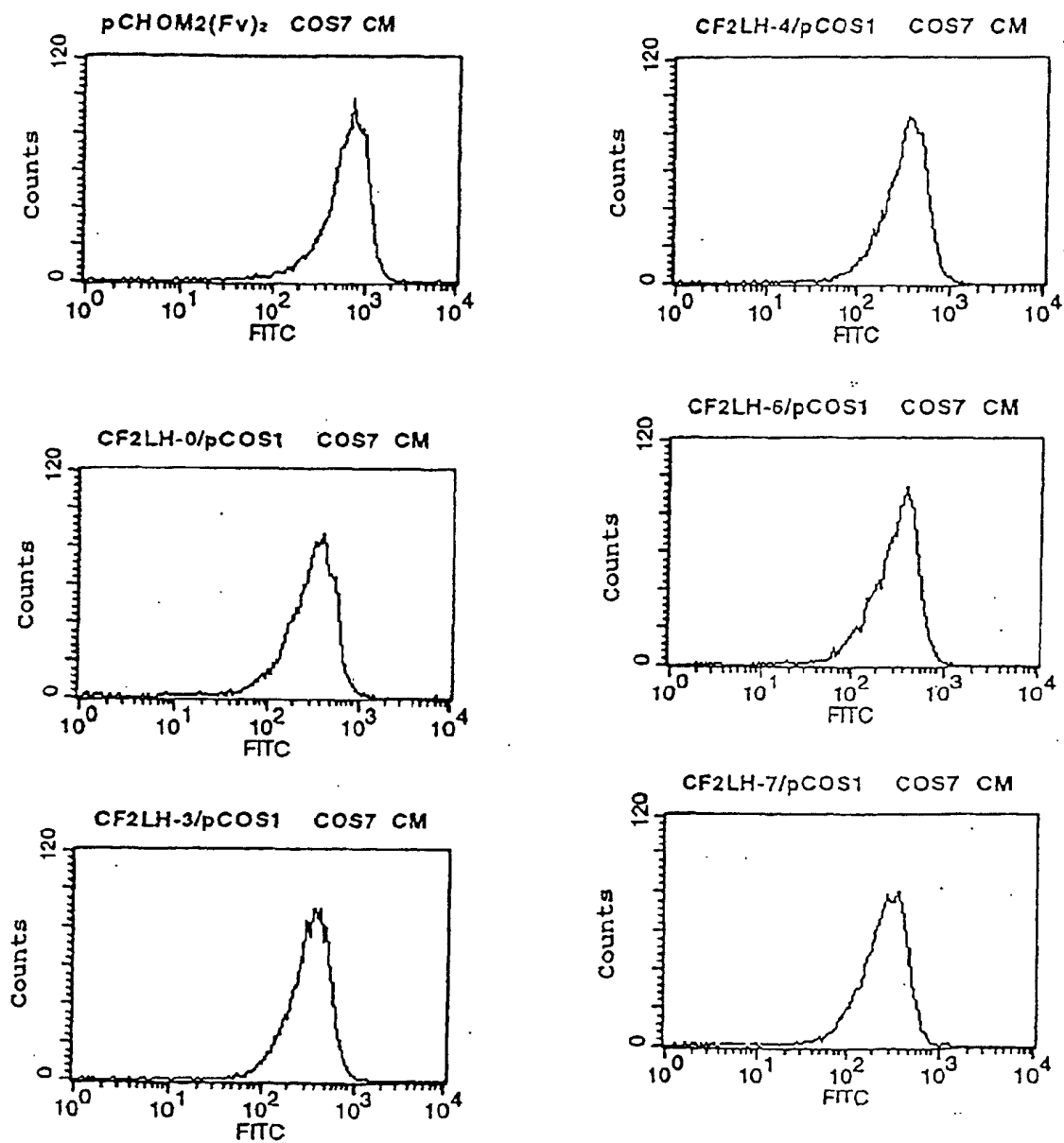


Fig. 41a

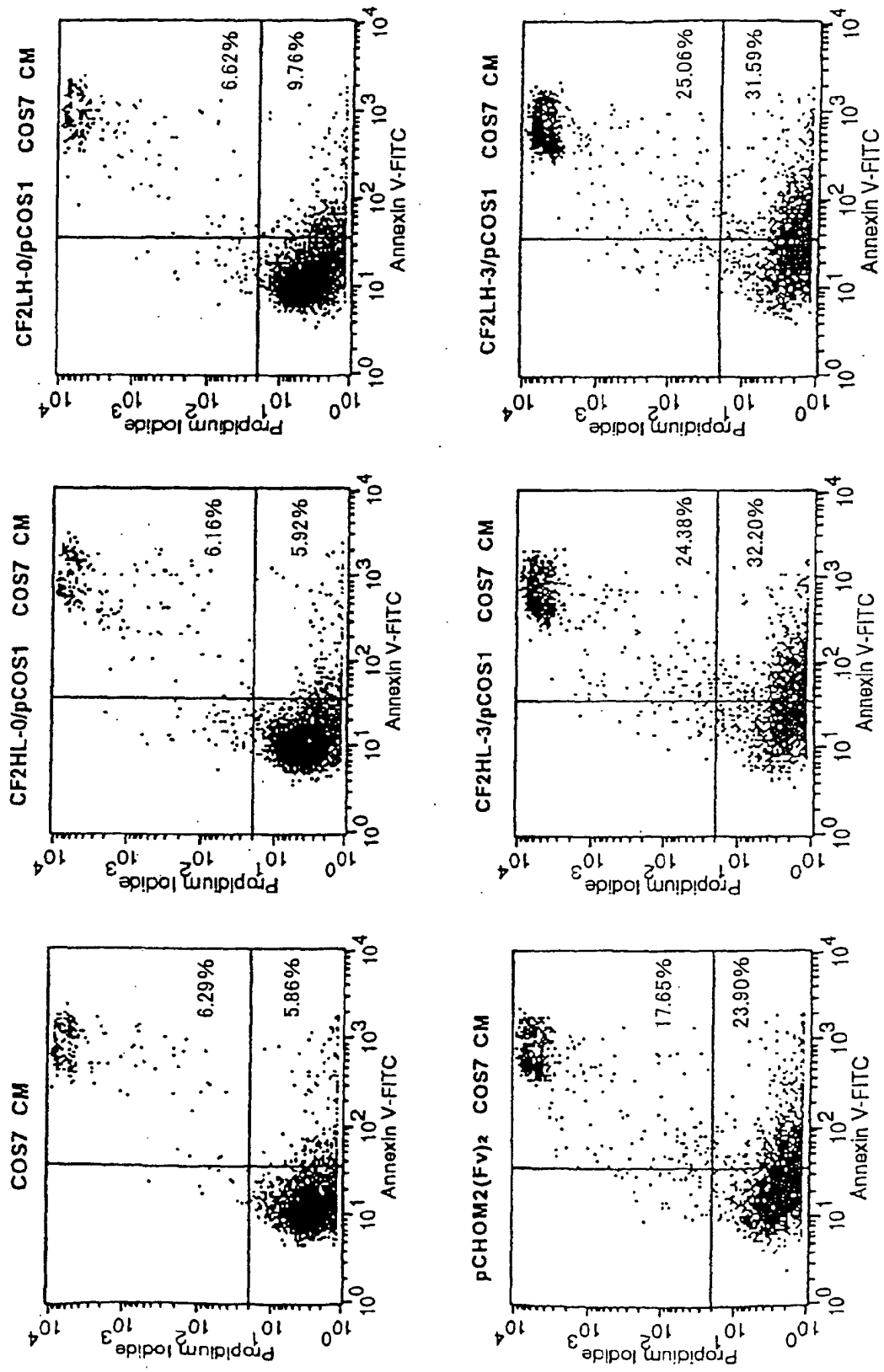


Fig. 41b

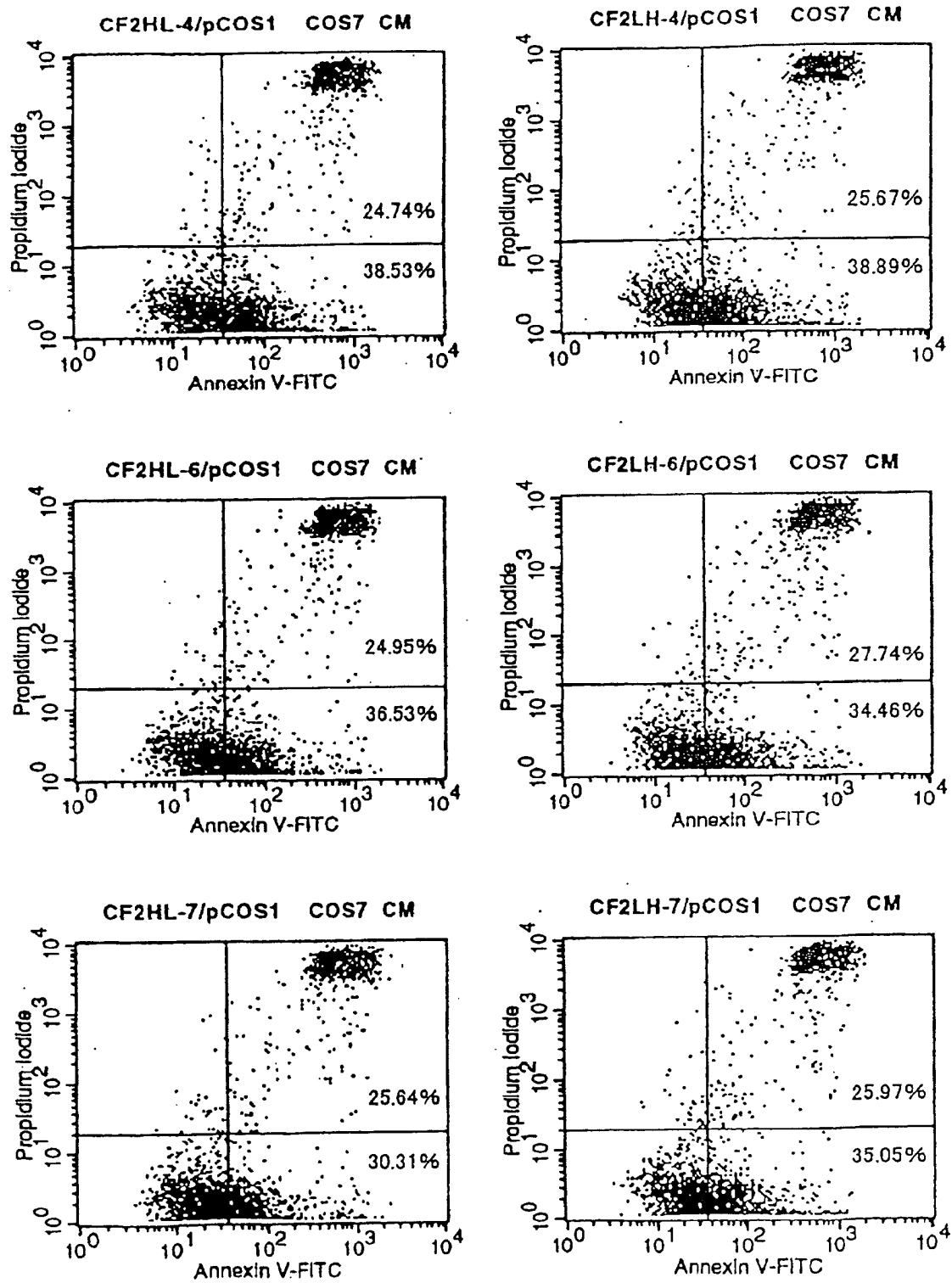


Fig. 42

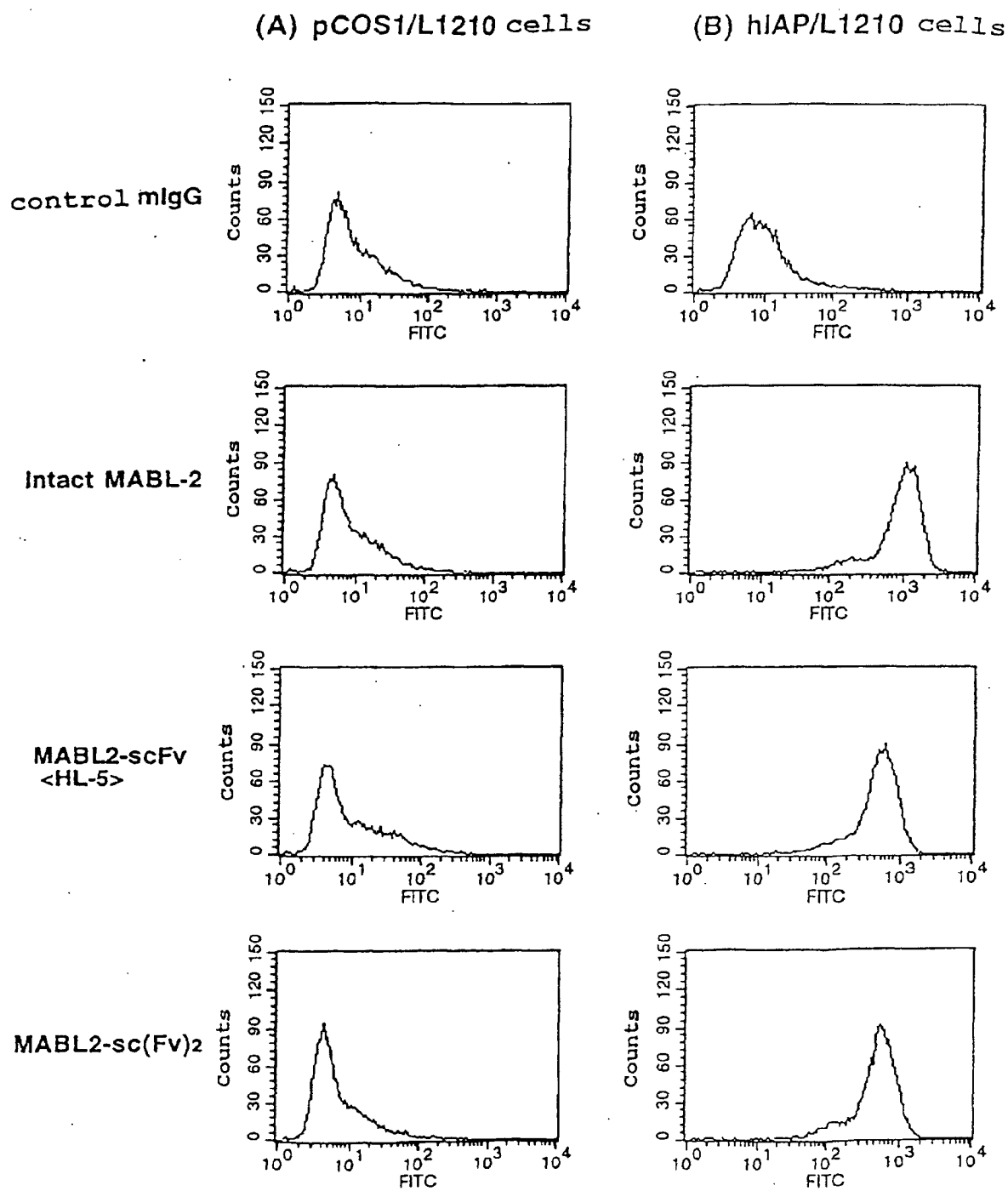


Fig. 43

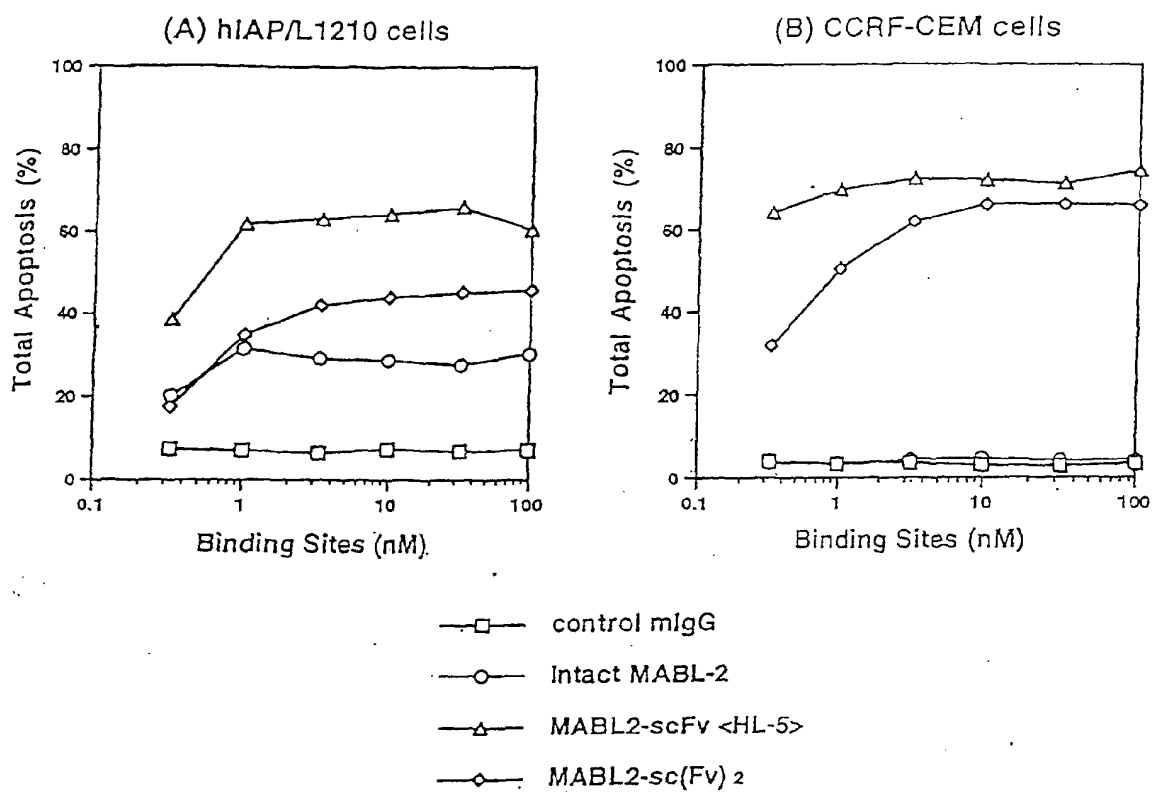


Fig. 44

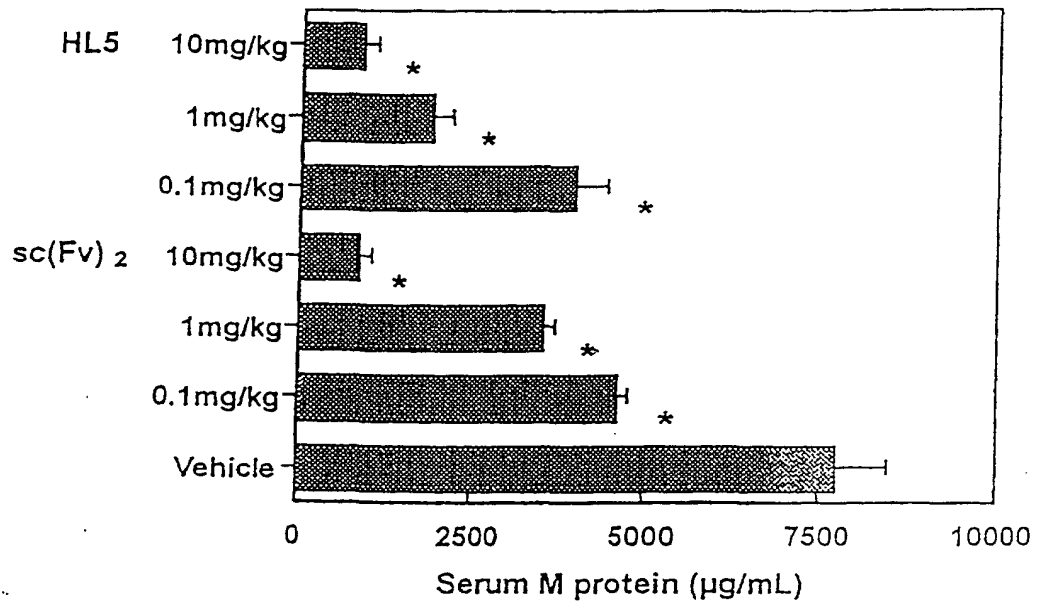


Fig. 45

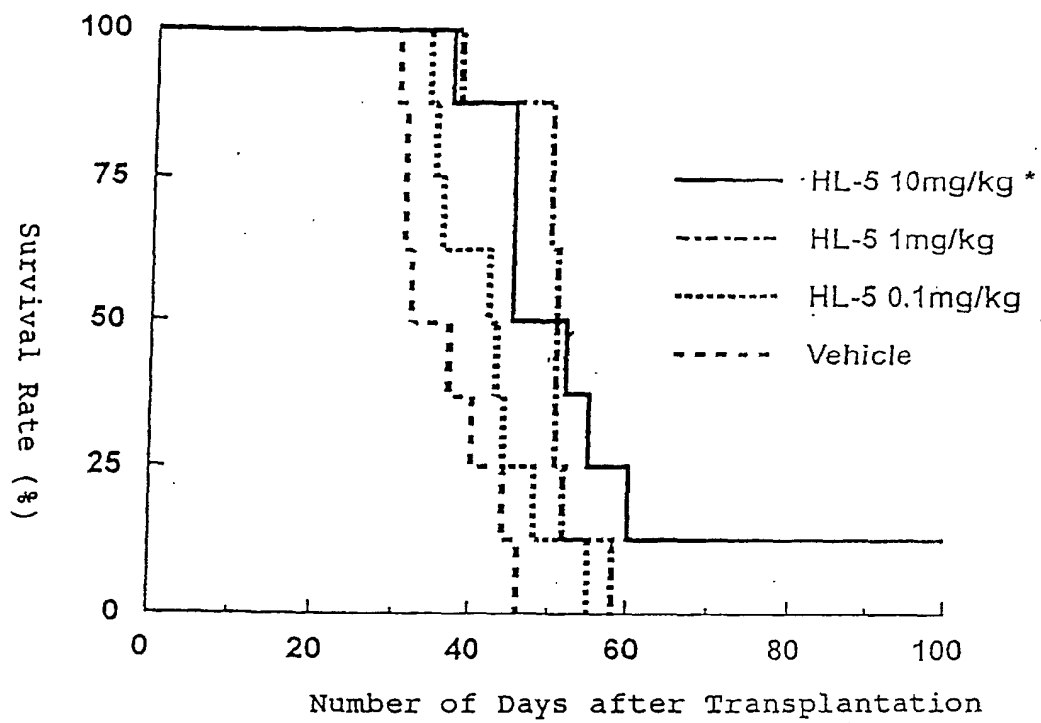


Fig. 46

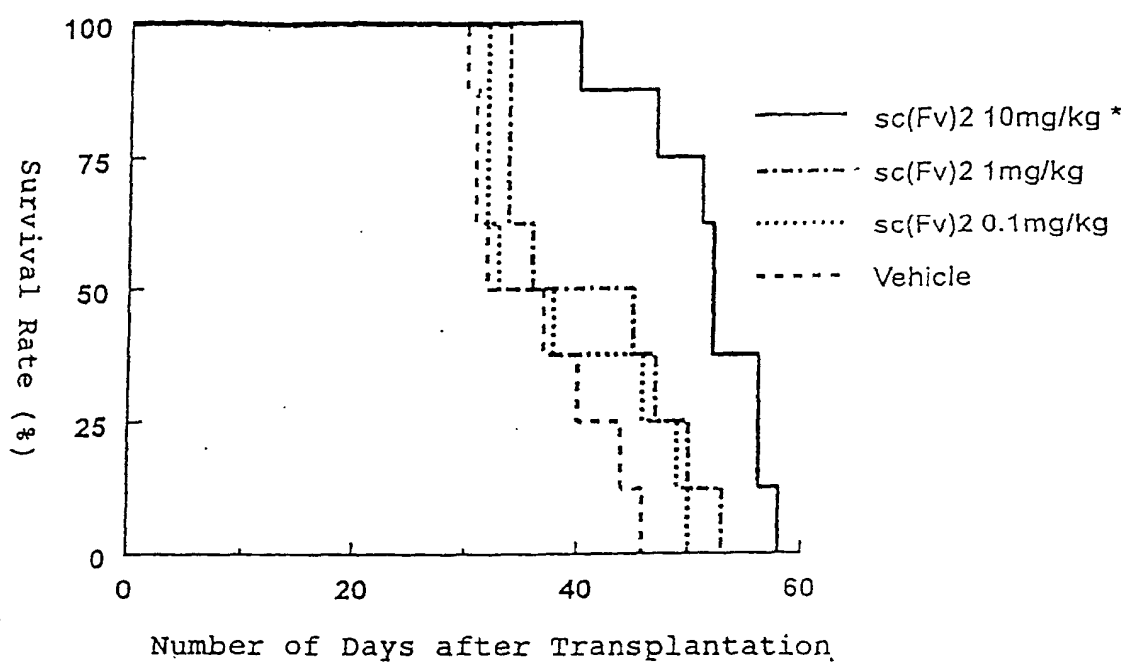


Fig. 47

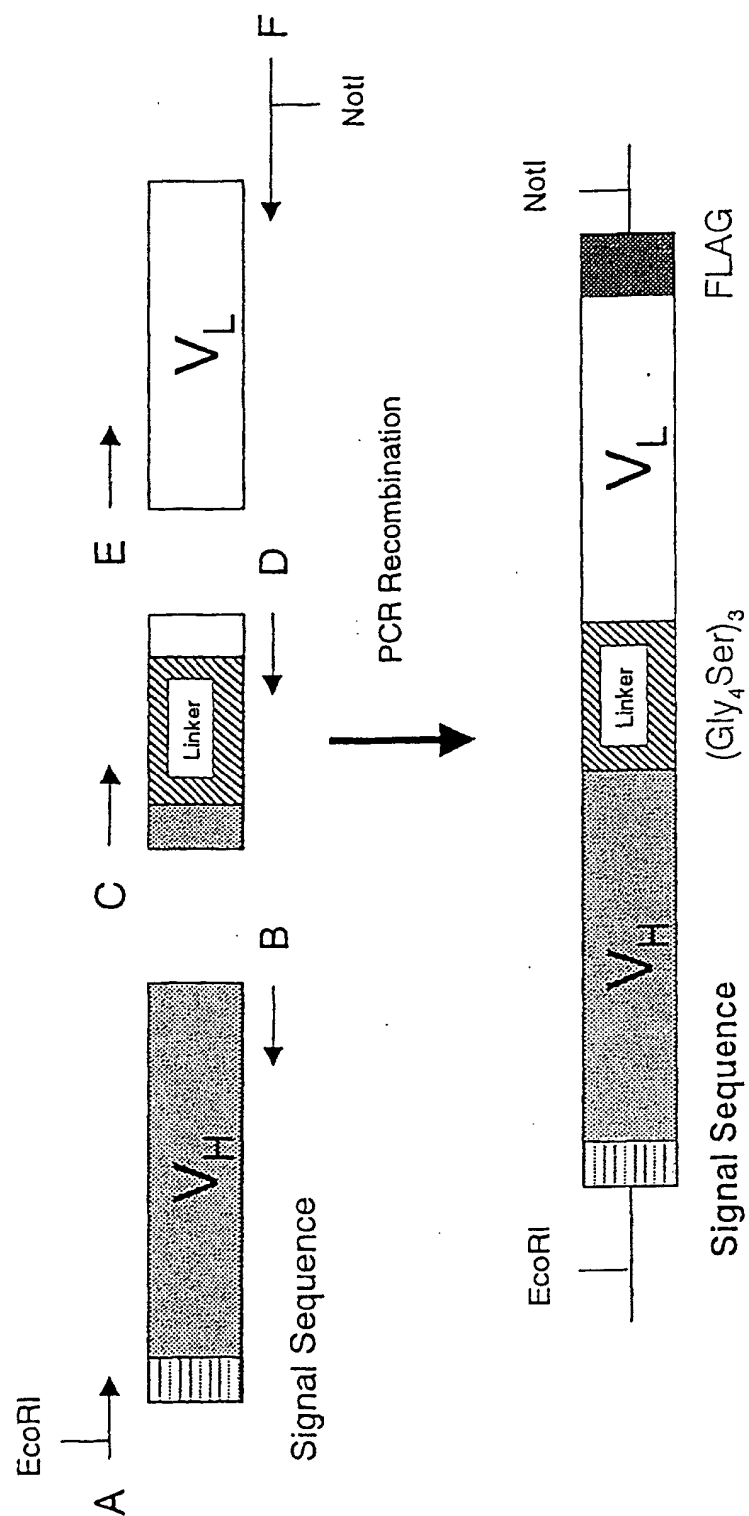


Fig. 48

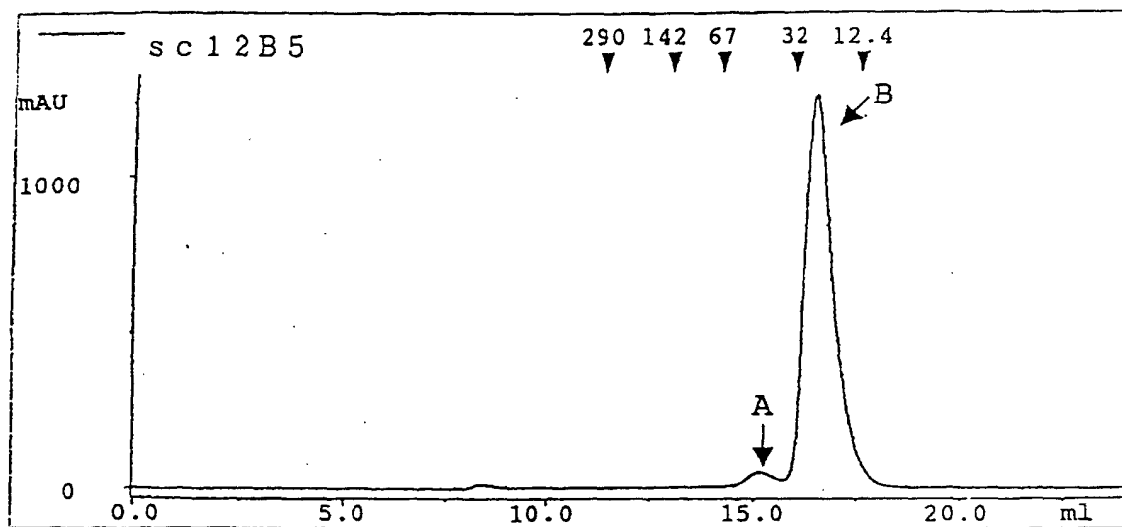


Fig. 49

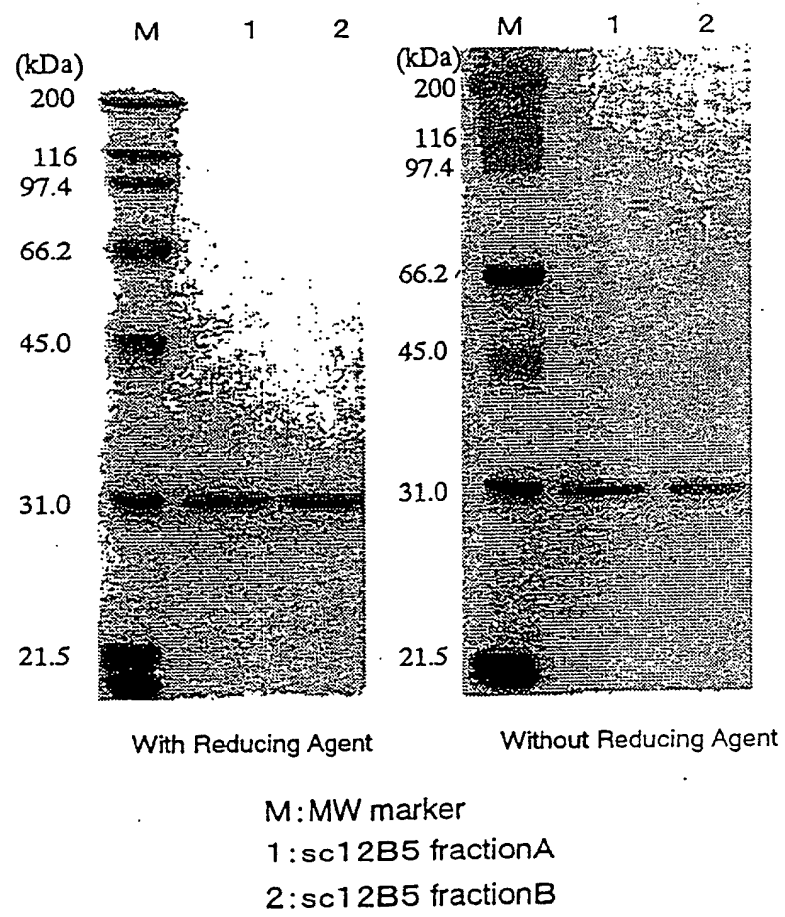


Fig. 50

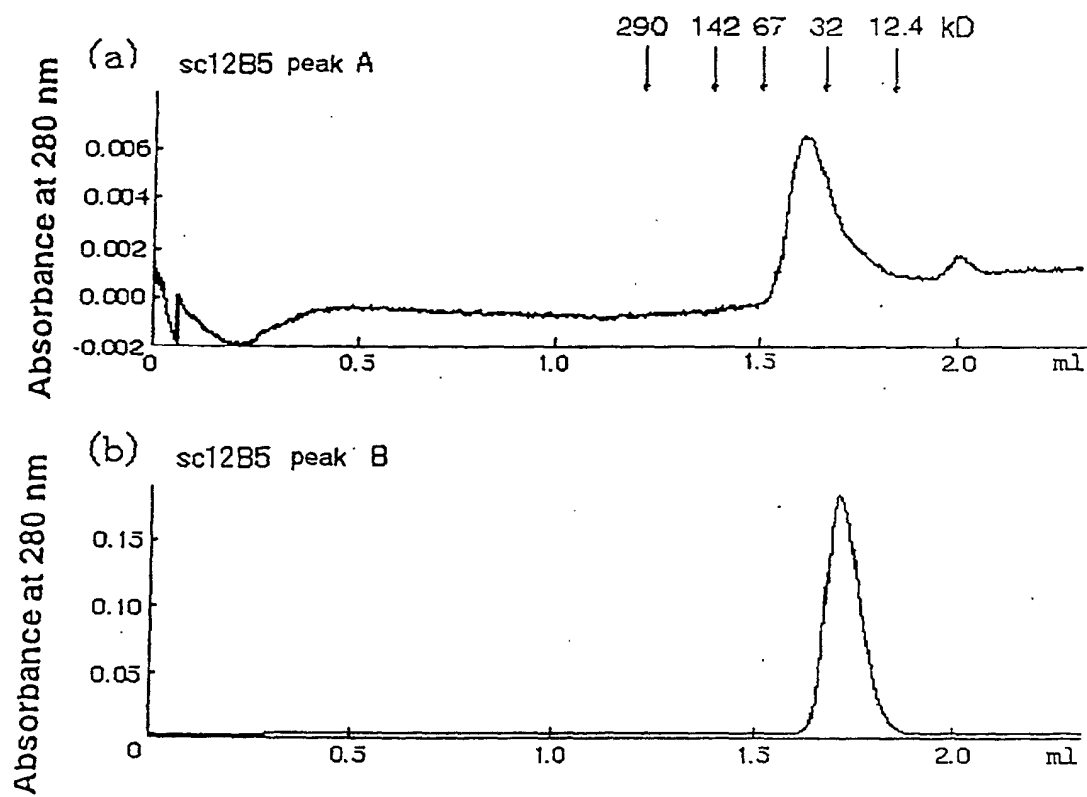


Fig. 51

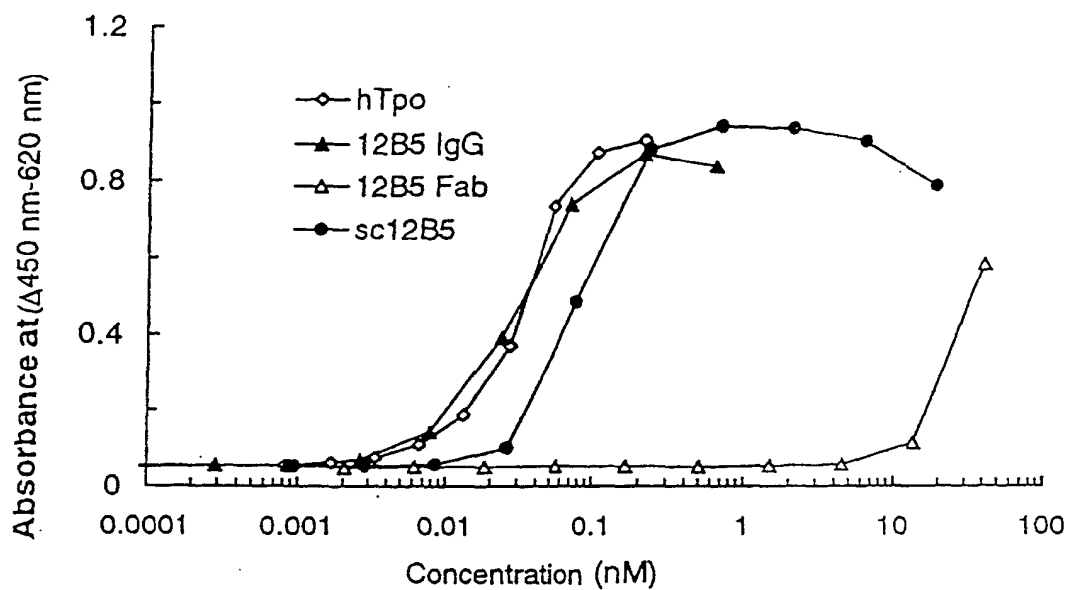


Fig. 52

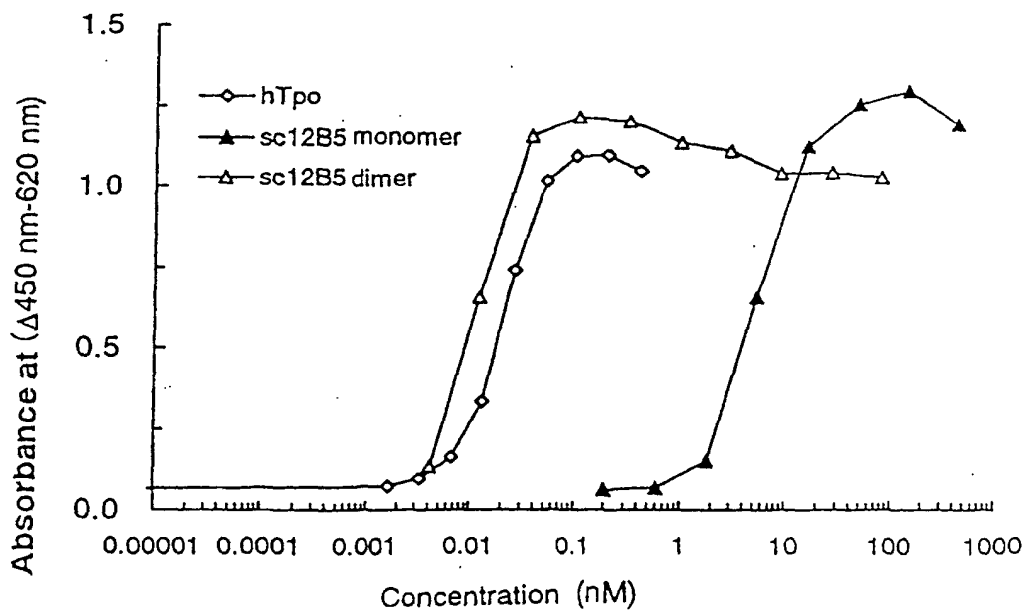


Fig. 53

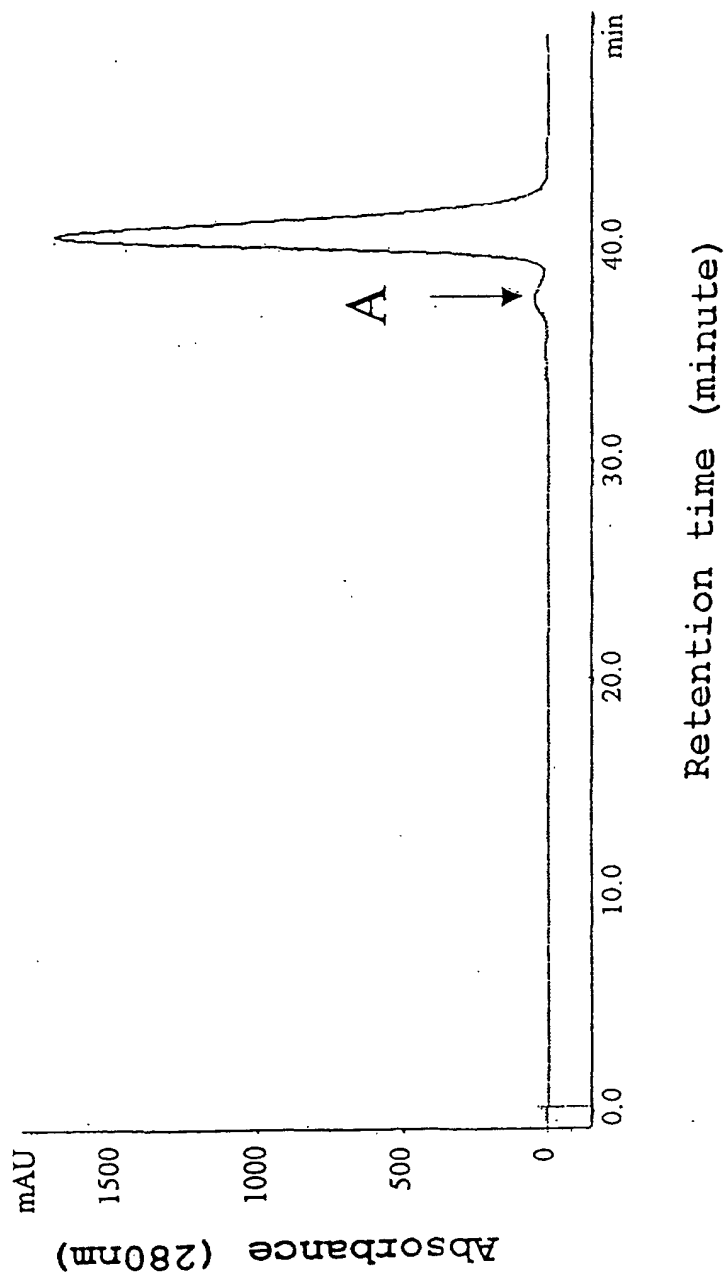


Fig. 54

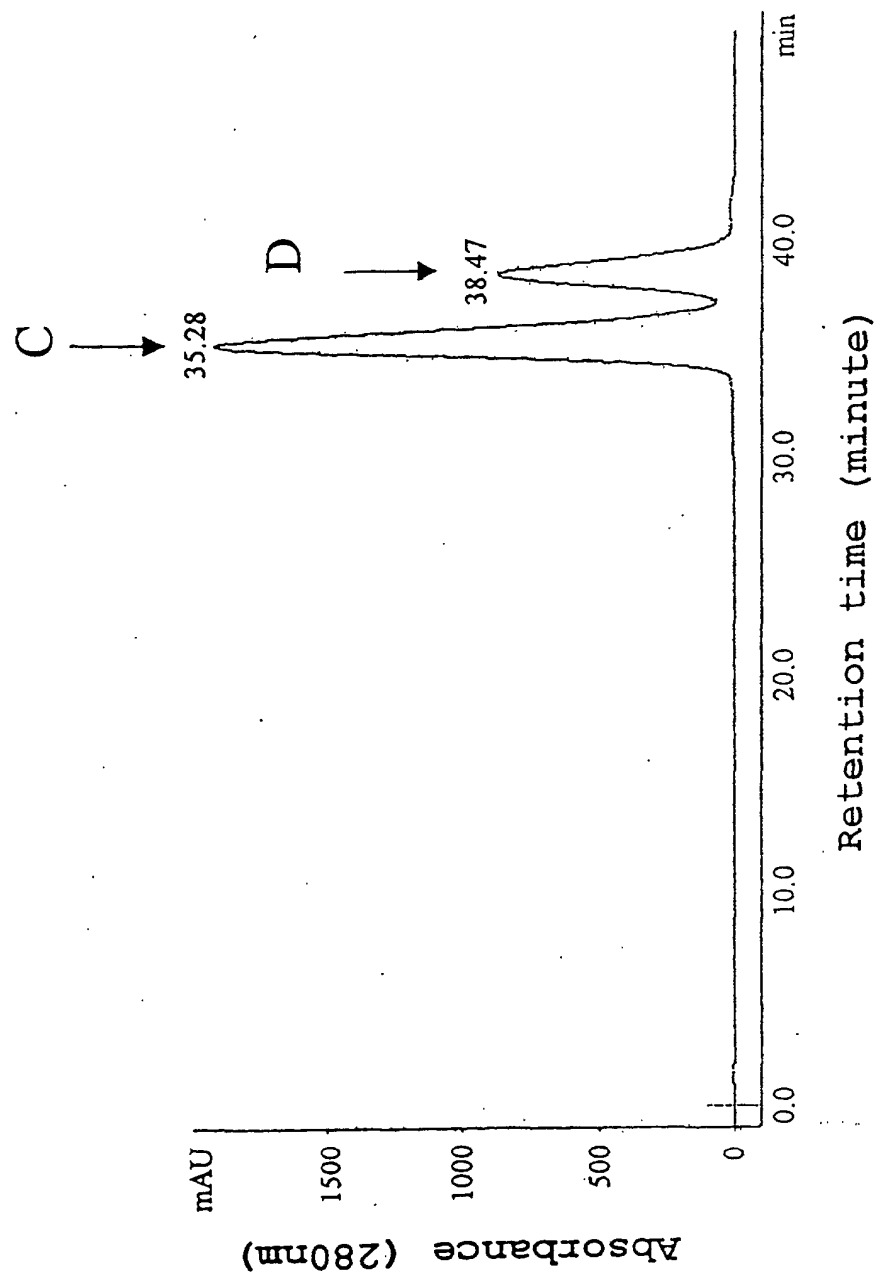


Fig. 5 5

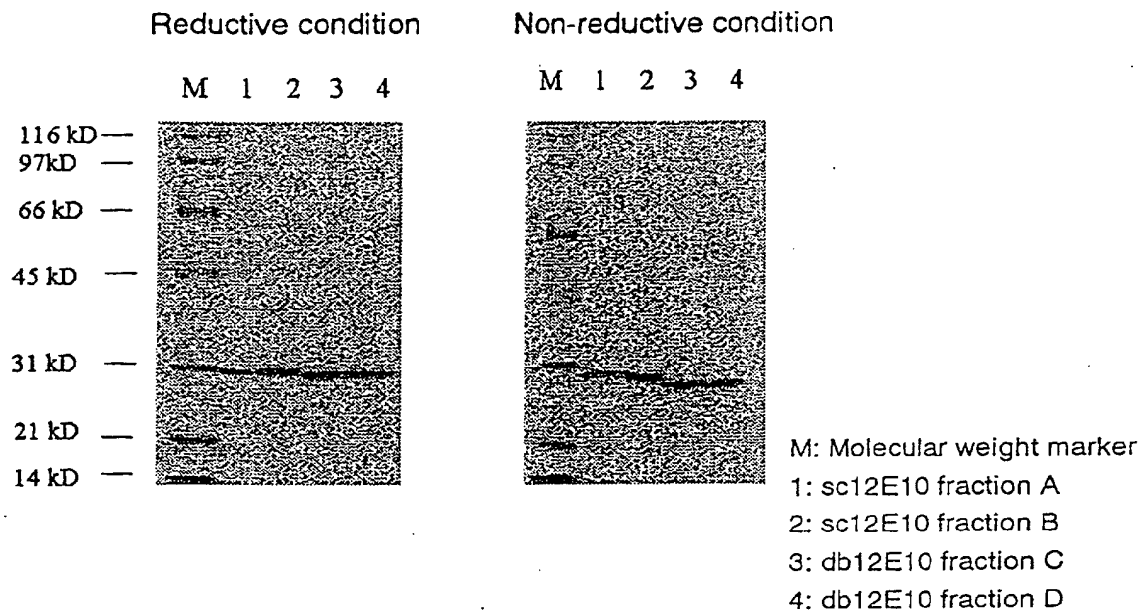


Fig. 56

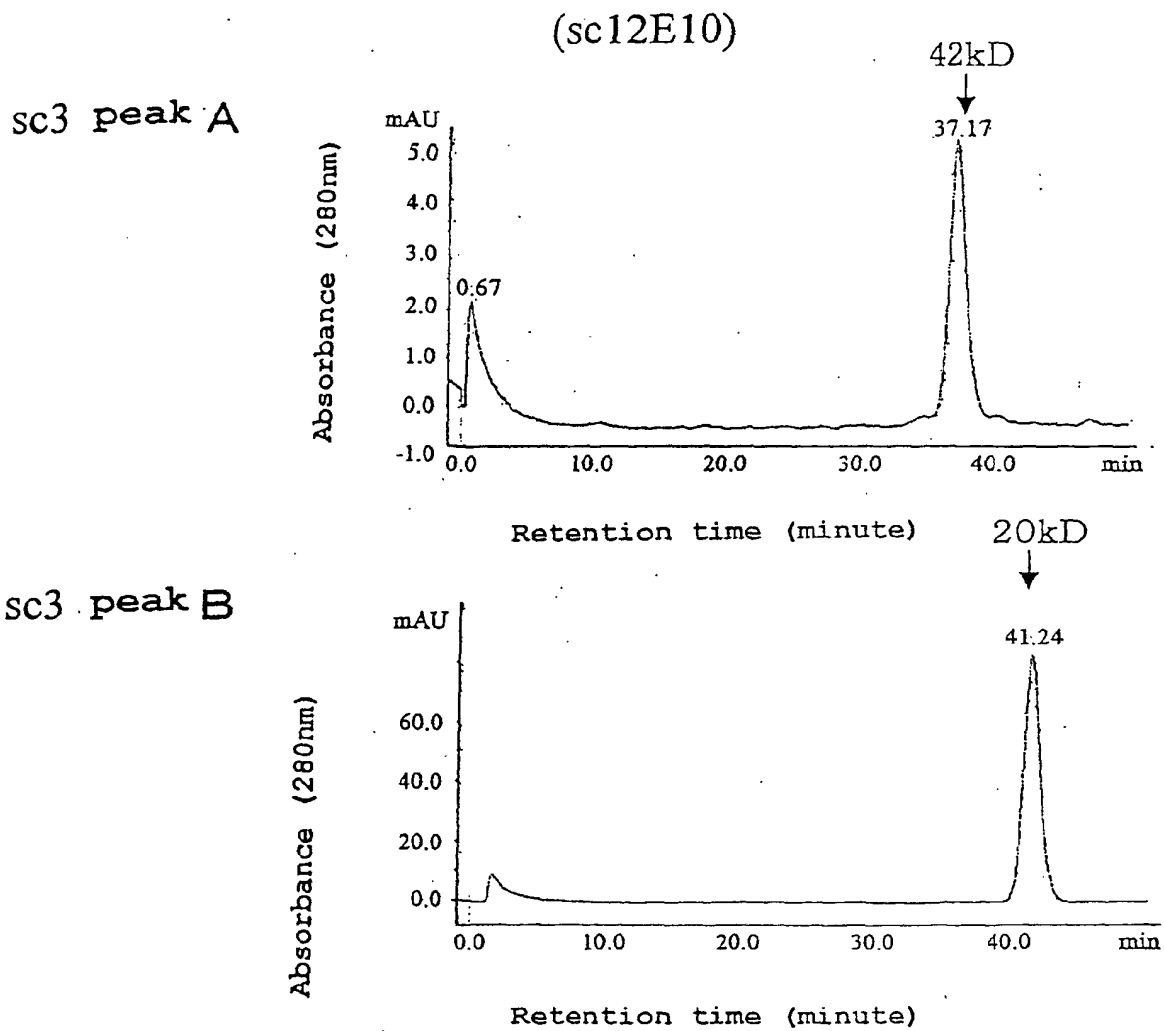


Fig. 57

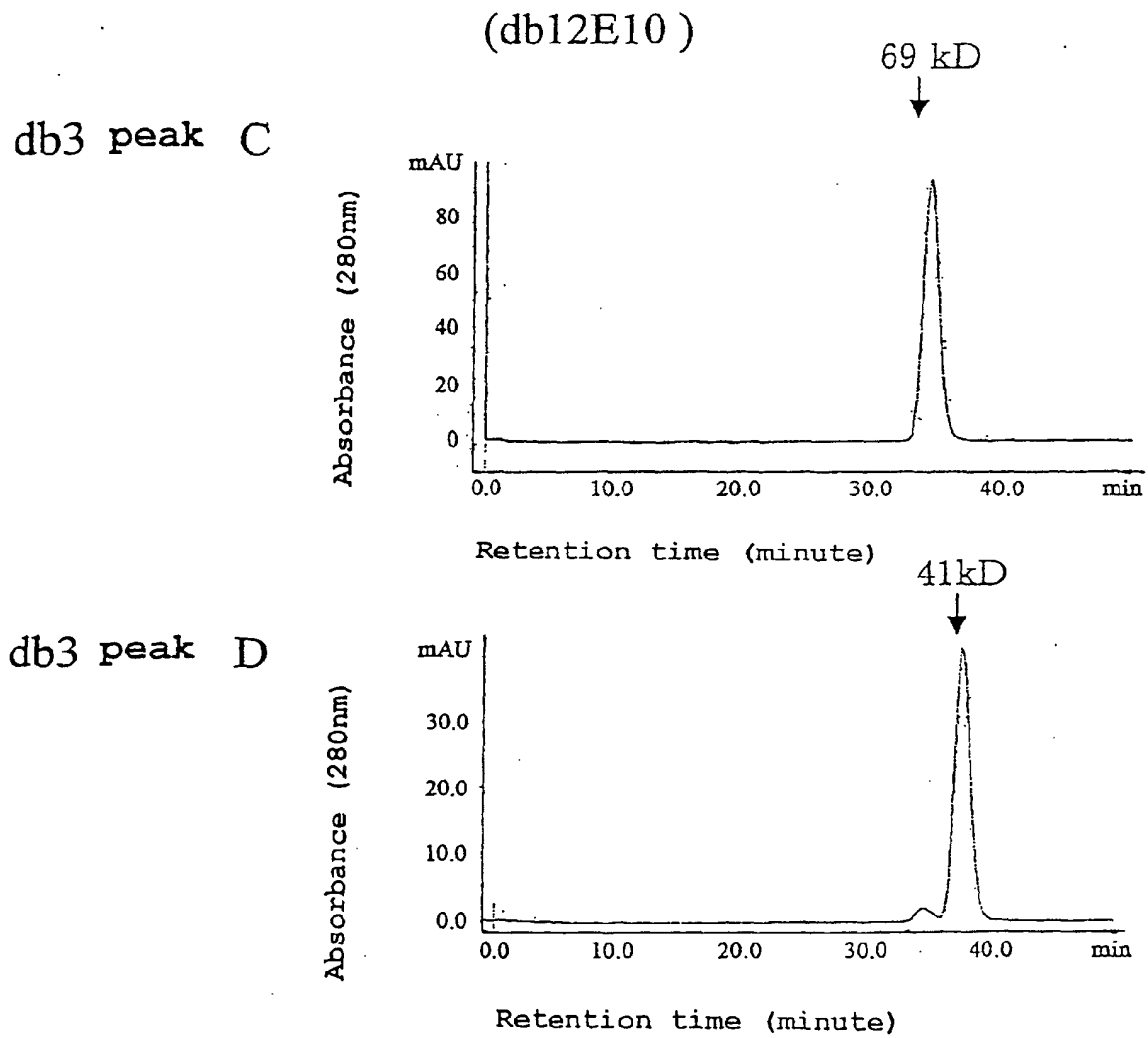


Fig. 5 8

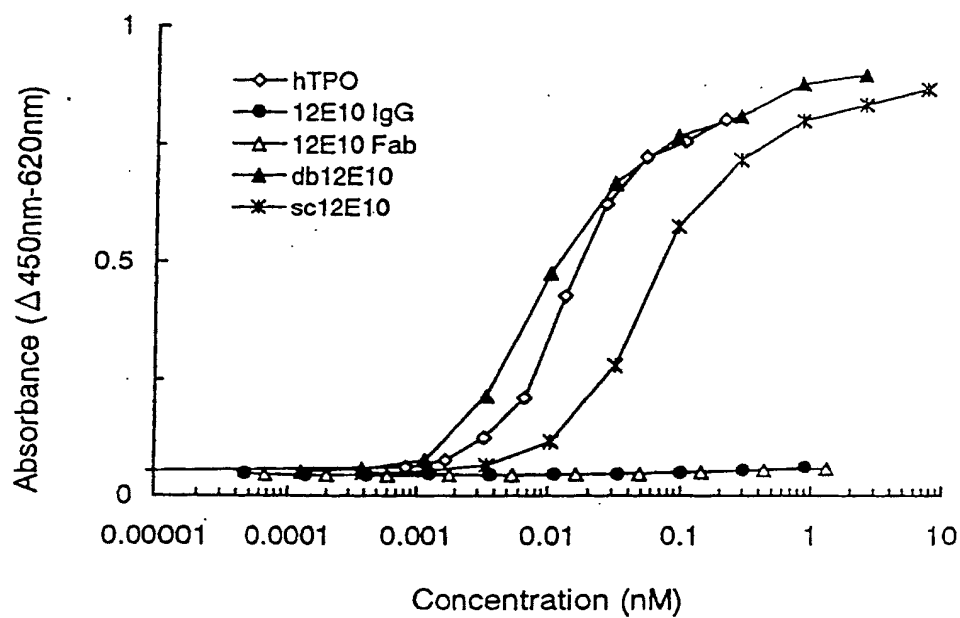
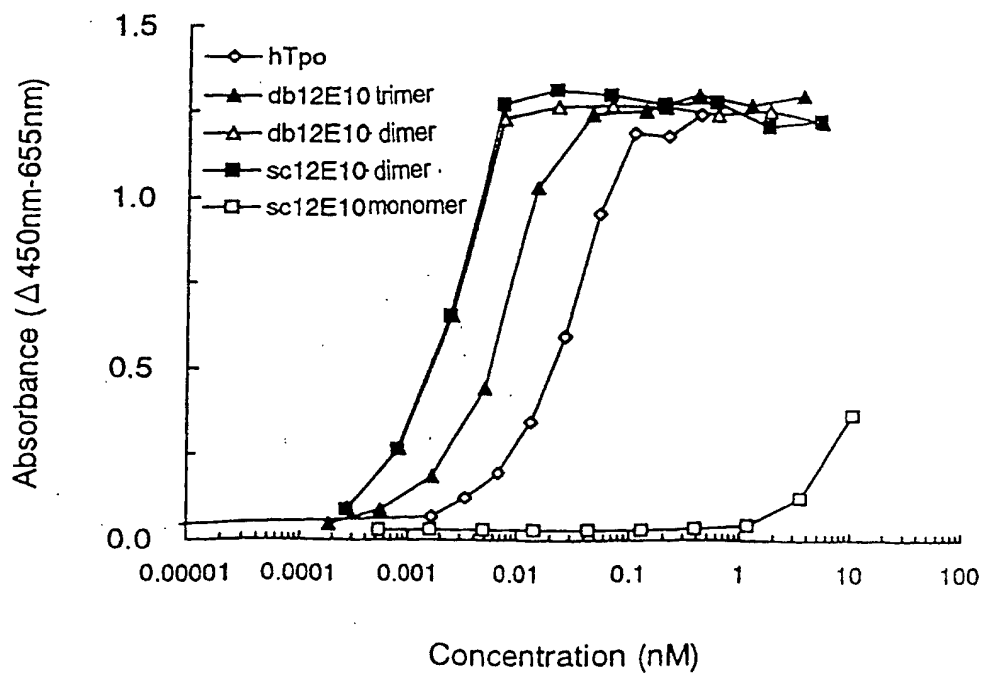


Fig. 5 9



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP01/09259

| A. CLASSIFICATION OF SUBJECT MATTER   |  |  |
|---|--|--|
| Int.Cl. <sup>7</sup> C12N15/09, 15/62, C07K16/28, A61K39/395  |  |  |
| According to International Patent Classification (IPC) or to both national classification and IPC   |  |  |
| B. FIELDS SEARCHED  |  |  |
| Minimum documentation searched (classification system followed by classification symbols)   |  |  |
| Int.Cl. <sup>7</sup> C12N15/09, 15/62, C07K16/28, A61K39/395  |  |  |
| Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched   |  |  |
| Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  |  |  |
| JICST FILE (JOIS), MEDLINE (STN), WPI (DIALOG), BIOSIS (DIALOG)   |  |  |
| C. DOCUMENTS CONSIDERED TO BE RELEVANT  |  |  |
| Category*   | Citation of document, with indication, where appropriate, of the relevant passages   | Relevant to claim No.  |
| Y   | Bijia DENG et al., "An Agonist Murine Monoclonal Antibody to the Human c-Mpl Receptor Stimulates Megakaryocytopoiesis", Blood, 15 September, 1998, Vol. 92, No. 6, pages 1981 to 1988                              | 1-40   |
| Y   | US 5885574 A (Amgen Inc.),<br>23 March, 1999 (23.03.99),<br>& JP 2000-95800 A & EP 773962 B1<br>& WO 96/03438 A  | 1-40   |
| Y   | KIPRIYANOV et al., "Bispecific CD3xCD19 Diabody for T Cell-Mediated Lysis of Malignant Human B Cells", Int. J. Cancer, (1998), Vol. 77, No. 5, pages 763 to 772  | 1-40   |
| Y   | WO 00/53634 A (Chugai Pharmaceutical Co., Ltd.),<br>14 September, 2000 (14.09.00),<br>& EP 1167388 A   | 1-40   |
| A   | Ming-Hong XIE et al., "Direct demonstration of MuSK involvement in acetylcholine receptor clustering through identification of agonist ScFv", Nature Biotechnology, August, 1997, Vol. 15, No. 8, pages 768 to 771 | 1-40   |
| <input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.  |  |  |
| * Special categories of cited documents:<br>"A" document defining the general state of the art which is not considered to be of particular relevance<br>"E" earlier document but published on or after the international filing date<br>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)<br>"O" document referring to an oral disclosure, use, exhibition or other means<br>"P" document published prior to the international filing date but later than the priority date claimed<br>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention<br>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone<br>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art<br>"&" document member of the same patent family |  |  |
| Date of the actual completion of the international search<br>29 January, 2002 (29.01.02)  |  | Date of mailing of the international search report<br>05 February, 2002 (05.02.02) |
| Name and mailing address of the ISA/<br>Japanese Patent Office  |  | Authorized officer   |
| Facsimile No.   |  | Telephone No.  |

Form PCT/ISA/210 (second sheet) (July 1992)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP01/09259

| C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT |  |                       |
|---|--|-----------------------|
| Category*   | Citation of document, with indication, where appropriate, of the relevant passages                   | Relevant to claim No. |
| A   | EP 1035132 A (Chugai Pharmaceutical Co., Ltd.),<br>13 September, 2000 (13.09.00),<br>& WO 99/12973 A | 1-40                  |

Form PCT/ISA/210 (continuation of second sheet) (July 1992)